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  NEWS 13  DEC 09   STN Entry Date available for display in REGISTRY and CA/CAplus
  NEWS 14  DEC 17   DGENE: Two new display fields added
  NEWS 15  DEC 18   BIOTECHNO no longer updated
  NEWS 16  DEC 19   CROPU no longer updated; subscriber discount no longer
                    available
  NEWS 17  DEC 22   Additional INPI reactions and pre-1907 documents added to CAS
                    databases
  NEWS 18  DEC 22   IFIPAT/IFIUDB/IFICDB reloaded with new data and search fields
  NEWS 19  DEC 22   ABI-INFORM now available on STN
  NEWS 20  JAN 27   Source of Registration (SR) information in REGISTRY updated
                    and searchable
  NEWS 21  JAN 27   A new search aid, the Company Name Thesaurus, available in
                    CA/CAplus
  NEWS 22  FEB 05   German (DE) application and patent publication number format
                    changes

  NEWS EXPRESS  DECEMBER 28 CURRENT WINDOWS VERSION IS V7.00, CURRENT
                MACINTOSH VERSION IS V6.0b(ENG) AND V6.0Jb(JP),
                AND CURRENT DISCOVER FILE IS DATED 23 SEPTEMBER 2003
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FULL ESTIMATED COST                                     0.21       0.21

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FILE COVERS 1971 TO PATENT PUBLICATION DATE: 19 Feb 2004 (20040219/PD)
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FILE LAST UPDATED: 19 Feb 2004 (20040219/ED)
HIGHEST GRANTED PATENT NUMBER: US6694518
HIGHEST APPLICATION PUBLICATION NUMBER: US2004034897
CA INDEXING IS CURRENT THROUGH 19 Feb 2004 (20040219/UPCA)
ISSUE CLASS FIELDS (/INCL) CURRENT THROUGH: 19 Feb 2004 (20040219/PD)
REVISED CLASS FIELDS (/NCL) LAST RELOADED: Dec 2003
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	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	1.35	1.56

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CA INDEXING COPYRIGHT (C) 2004 AMERICAN CHEMICAL SOCIETY (ACS)

FILE COVERS 1971 TO PATENT PUBLICATION DATE: 19 Feb 2004 (20040219/PD)
FILE LAST UPDATED: 19 Feb 2004 (20040219/ED)
HIGHEST GRANTED PATENT NUMBER: US6694518
HIGHEST APPLICATION PUBLICATION NUMBER: US2004034897
CA INDEXING IS CURRENT THROUGH 19 Feb 2004 (20040219/UPCA)
ISSUE CLASS FIELDS (/INCL) CURRENT THROUGH: 19 Feb 2004 (20040219/PD)
REVISED CLASS FIELDS (/NCL) LAST RELOADED: Dec 2003
USPTO MANUAL OF CLASSIFICATIONS THESAURUS ISSUE DATE: Dec 2003

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>>> publication date for all the US publications for an invention <<<
>>> are displayed in the PI (Patent Information) field of USPATFULL <<<
>>> records and may be searched in standard search fields, e.g., /PN, <<<
>>> /PK, etc. <<<

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>>> Use USPATALL when searching terms such as patent assignees, <<<
>>> classifications, or claims, that may potentially change from <<<

>>> the earliest to the latest publication. <<<

This file contains CAS Registry Numbers for easy and accurate substance identification.

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=> e brust stefan/in
E1            1     BRUST RUEDIGER/IN
E2            1     BRUST RUSSELL E/IN
E3           13 --> BRUST STEFAN/IN
E4           16     BRUST THOMAS B/IN
E5            3     BRUST THOMAS E/IN
E6            1     BRUST WILLI/IN
E7            1     BRUSTAD GEORG/IN
E8            2     BRUSTAD JOHN/IN
E9            7     BRUSTAD JOHN R/IN
E10           1     BRUSTAD JOHN T/IN
E11           2     BRUSTAD VAL G/IN
E12           1     BRUSTAD WAYNE L/IN

=> s e3
L1           13 "BRUST STEFAN"/IN

=> d l1,ti,1-13

L1   ANSWER 1 OF 13  USPATFULL on STN
TI     Retrovirus from the HIV group and its use

L1   ANSWER 2 OF 13  USPATFULL on STN
TI     Retrovirus from the HIV type O and its use (MVP-2901/94)

L1   ANSWER 3 OF 13  USPATFULL on STN
TI     Peptides derived from a retrovirus of the HIV group and their use

L1   ANSWER 4 OF 13  USPATFULL on STN
TI     METHOD OF DETECTING NUCLEIC ACID ENCODING A RETROVIRUS USING POLYMERASE
       CHAIN REACTION (PCR)

L1   ANSWER 5 OF 13  USPATFULL on STN
TI     Retrovirus from the HIV group and its use (MVP-2901/94)

L1   ANSWER 6 OF 13  USPATFULL on STN
TI     Immunochemical determination of multivalent analytes

L1   ANSWER 7 OF 13  USPATFULL on STN
TI     Increasing the sensitivity in the immunochemical determination of an
       analyte

L1   ANSWER 8 OF 13  USPATFULL on STN
TI     Immunodissociation for improving the immunochemical determination of an
       analyte

L1   ANSWER 9 OF 13  USPATFULL on STN
TI     Process for the immunochemical determination of an analyte

L1   ANSWER 10 OF 13  USPATFULL on STN
TI     Artificial positive controls derived from bifunctional conjugates

L1   ANSWER 11 OF 13  USPATFULL on STN
TI     Peptides derived from a retrovirus of the HIV group and their use

L1   ANSWER 12 OF 13  USPATFULL on STN
TI     Retrovirus from the HIV type O and its use (MVP-2901/94)

L1   ANSWER 13 OF 13  USPATFULL on STN
TI     Artificial positive controls derived from bifunctional conjugates
```

=> d l1,cbib,ab,clm,1-5,11,12

L1 ANSWER 1 OF 13 USPATFULL on STN
2003:213280 Retrovirus from the HIV group and its use.
Hauser, Hans-Peter, Marburg, GERMANY, FEDERAL REPUBLIC OF
Knapp, Stefan, Marburg, GERMANY, FEDERAL REPUBLIC OF
Brust, Stefan, Marburg, GERMANY, FEDERAL REPUBLIC OF
Gurtler, Lutz G., Munchen, GERMANY, FEDERAL REPUBLIC OF
Eberle, Josef, Freising, GERMANY, FEDERAL REPUBLIC OF
Kaptue, Lazare, Yaounde/Cameroun, GERMANY, FEDERAL REPUBLIC OF
Zekeng, Leopold Achenqui, Yaounde/Cameroun, GERMANY, FEDERAL REPUBLIC OF
US 2003147917 A1 20030807
APPLICATION: US 2003-357400 A1 20030204 (10)
PRIORITY: DE 1995-19505262 19950216
DOCUMENT TYPE: Utility; APPLICATION.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB A novel immunodeficiency virus is disclosed which has the designation MVP-2901/94 and which has been deposited with the European Collection of Animal Cell Cultures (ECACC) under No. V 95012601. The characteristic antigens which can be obtained from the virus and which can be employed for detecting antibodies against retroviruses which are associated with immunodeficiency diseases are also disclosed, as are the partial DNA and amino acid sequences of the virus.

CLM What is claimed is:

1. An isolated virus which has the morphological and immunological properties of retrovirus MVP-2901/94.

2. The isolated virus of claim 1, wherein said virus is a retrovirus, the genome of which is at least 75% homologous to the genome of retrovirus MVP-290/94.

3. The isolated virus of claim 2, the genome of which is at least 85% homologous to the genome of retrovirus MVP-2901/94.

4. The isolated retrovirus of claim 3, the genome of which is at least 90% homologous to the genome of retrovirus MVP 2901/94.

5. Isolated virus MVP 2901/94.

6. An isolated nucleic acid molecule which is complementary to the RNA or parts thereof, of the isolated virus of claim 1.

7. An isolated protein or polypeptide encoded by the isolated virus of claim 1.

8. An isolated peptide consisting of at least 10 amino acids found in a linear array of the isolated protein or polypeptide of claim 1.

9. The isolated peptide of claim 8, consisting of at least 20 amino acids.

10. The isolated peptide of claim 8, wherein said at least 10 amino acids are a linear array of 10 amino acids of SEQ ID NO: 3.

11. Test kit useful in determining presence of a virus in a sample, comprising the isolated protein or polypeptide of claim 7, and a substance which specifically binds to an antibody which binds to said virus.

12. Test kit useful in determining presence of a virus in a sample, comprising the isolated peptide of claim 8, and a substance which specifically binds to an antibody which binds to said virus.

13. The test kit of claim 11, wherein said substance is protein A.

14. The test kit of claim 11, wherein said substance is an antibody.

15. The test kit of claim 12, wherein said substance is protein A.

16. The test kit of claim 12, wherein said substance is an antibody.

17. The test kit of claim 11, wherein said substance is labelled with an enzyme or a fluorescent molecule.

18. The test kit of claim 12, wherein said first antibody is labelled with an enzyme or a fluorescent molecule.

19. Method for determining a virus in a sample, comprising contacting said sample with the protein or polypeptide of claim 7 and determining binding of any antibody in said sample to said protein or polypeptide as a determination of virus in said sample.

20. The method of claim 19, further comprising contacting said sample with a second antibody which binds to said antibody.

21. Method for determining a virus in a sample, comprising contacting said sample with the peptide of claim 8 and determining binding of antibodies in said sample to said peptide as a determination of virus in said sample.

22. The method of claim 21, further comprising contacting said sample with an antibody which binds to said antibodies, and determining binding therebetween.

23. An isolated nucleic acid molecule which hybridizes to a portion of the isolated virus of claim 1, consisting of from 10 to 50 nucleotides.

24. The isolated nucleic acid molecule of claim 23, consisting of from 10 to 25 nucleic acid.

25. The isolated nucleic acid molecule of claim 24, consisting of from 12 to 18 nucleotides.

26. Method for determining presence of a virus in a sample, comprising contacting said sample with the isolated nucleic acid molecule of claim 23 and determining hybridization of said isolated nucleic acid molecule to said virus as a determination of said virus in said sample.

27. Method for determining presence of a virus in a sample, comprising contacting said sample with the isolated nucleic acid molecule of claim 23 hybridizing said isolated nucleic acid molecule to said virus, amplifying said isolated nucleic acid molecule to produce an amplification product, and determining said amplification product as a determination of said virus in said sample.

L1 ANSWER 2 OF 13 USPATFULL on STN
2003:102445 Retrovirus from the HIV type O and its use (MVP-2901/94).
Hauser, Hans-Peter, Marburg, GERMANY, FEDERAL REPUBLIC OF
Knapp, Stefan, Marburg, GERMANY, FEDERAL REPUBLIC OF
Brust, Stefan, Marburg, GERMANY, FEDERAL REPUBLIC OF
Gurtler, Lutz G., Munich, GERMANY, FEDERAL REPUBLIC OF
Eberle, Josef, Freising, GERMANY, FEDERAL REPUBLIC OF
Kaptue, Lazare, Yaounde/Cameroun, GERMANY, FEDERAL REPUBLIC OF
Zekeng, Leopold Achengui, Yaounde/Cameroun, GERMANY, FEDERAL REPUBLIC OF
Dade Behring Marburg GmbH, Marburg, GERMANY, FEDERAL REPUBLIC OF (non-U.S. corporation)
US 6548635 B1 20030415
APPLICATION: US 2000-610271 20000706 (9)
PRIORITY: DE 1995-19505262 19950216
DOCUMENT TYPE: Utility; GRANTED.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB A novel HIV type O immunodeficiency virus is disclosed which has the designation MVP-2901/94 and which has been deposited with the European Collection of Animal Cell Cultures (ECACC) under No. V 950121601. The characteristic antigens which can be obtained from the virus and which can be employed for detecting antibodies against retroviruses which are associated with immunodeficiency diseases are also disclosed, as are the partial DNA and amino acid sequences of the virus.

CLM What is claimed is:

1. An isolated protein or polypeptide encoded by an isolated virus wherein said isolated protein or polypeptide binds with an antibody that binds to a polypeptide consisting of the amino acid sequence of positions 319-341 in SEQ ID NO: 12.

2. An isolated peptide consisting of at least 10 contiguous amino acids of the isolated protein or polypeptide of claim 1 wherein the isolated peptide binds with an antibody that binds to the polyepeptide consisting of the amino acid sequence of positions 319-341 in SEQ ID NO: 12.

3. The isolated peptide of claim 2, consisting of at least 20 amino acids.

4. The isolated peptide of claim 2, wherein said at least 10 contiguous amino acids are 10 contiguous amino acids of SEQ ID NO: 12.

5. A test kit for detecting the presence of a virus in a sample, comprising the isolated peptide of claim 2, and a substance which specifically binds to an antibody which binds to said peptide.

6. The test kit of claim 5, wherein said substance is protein A.

7. The test kit of claim 5, wherein said substance is an antibody.

8. The test kit of claim 5, wherein said antibody is labeled with an enzyme or a fluorescent molecule.

9. A test kit for detecting the presence of a virus in a sample, comprising the isolated protein or polypeptide of claim 1, and a substance which specifically binds to an antibody which binds to said isolated protein or polypeptide.

10. The test kit of claim 9, wherein said substance is protein A.

11. The test kit of claim 9, wherein said substance is an antibody.

12. The test kit of claim 9, wherein said substance is labeled with an enzyme or a fluorescent molecule.

13. A test kit for detecting an antibody which binds with human immunodeficiency virus in a sample, comprising (1) a polypeptide comprising the amino acid sequence set forth in SEQ ID NO:12 and (2) a substance which specifically binds to an antibody which binds to said polypeptide.

14. The test kit of claim 13, wherein the polypeptide consists of the amino acid sequence set forth in SEQ ID NO: 12.

15. A test kit for detecting an antibody that binds to human immunodeficiency virus in a sample, said kit comprising (1) an isolated virus that binds to antibodies that bind to a polypeptide consisting of the amino acid sequence at positions 319-341 in SEQ ID NO: 12 and (2) a substance which specifically binds to the antibody that binds to the isolated virus.

16. The test kit of claim 15, wherein said isolated virus is MVP-2901/94.

L1 ANSWER 3 OF 13 USPATFULL on STN
2002:227886 Peptides derived from a retrovirus of the HIV group and their use.
Brust, Stefan, Marburg-Michelbach, GERMANY, FEDERAL REPUBLIC OF
Knapp, Stefan, Marburg, GERMANY, FEDERAL REPUBLIC OF
Gerken, Manfred, Marburg, GERMANY, FEDERAL REPUBLIC OF
Guertler, Lutz G., Muenchen, GERMANY, FEDERAL REPUBLIC OF
US 2002123039 A1 20020905
APPLICATION: US 2001-321 A1 20011204 (10)
PRIORITY: DE 1994-4405810 19940223
DOCUMENT TYPE: Utility; APPLICATION.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Immunologically active peptides which are derived from a novel immunodeficiency virus which has the designation MVP5180/91 are described. A diagnostic composition containing such a peptide and methods of detecting an antibody against a retrovirus that causes immune deficiency using such diagnostic composition are also described. A kit containing the immunologically active peptides is also described. An immunogen and method of immunizing a mammal against HIV infection using the immunologically active peptides is described. DNA encoding the peptides and methods of detecting nucleic acids encoding HIV viruses are also described.
CLM What is claimed is:
1. An immunologically active peptide comprising at least 15 consecutive amino acids selected from the amino acids in the following sequence: VWGIRQLRARLQALETLIQNQQRLNLWGXKGKLIXYTSVKWNTSWSGR, wherein X is C or S.

2. The peptide of claim 1, wherein said at least 15 consecutive amino acids are selected from the amino acids in the following amino acid sequence: RLQALETLIQNQQRLNLWGXKGKLIXYTSVKWN wherein X is C or S.

3. The peptide of claim 1 which binds antibodies against retroviruses of the HIV type.

4. The peptide of claim 1 comprising from 20 to 30 consecutive amino acids.

5. The peptide of claim 1 which further comprises, at one or both ends of the peptide, one or more sequences of amino acids, wherein said sequences are not taken from the amino acid sequence of the retrovirus MVP5180/91.

6. The peptide of claim 1, wherein X is C.

7. The peptide of claim 6, wherein C represents a cysteine residue in an oxidized state.

8. The peptide of claim 6 comprising the amino acid sequence RLQALETLIQNQQRLNLWGCKGKLIC.

9. The peptide of 8, wherein C represents a cysteine residue in an oxidized state.

10. The peptide of claim 6 comprising the amino acid sequence NQQRLNLWGCKGKLICYTSVKNW.

11. The peptide of claim 10, wherein C represents a cysteine residue in an oxidized state.

12. The peptide of claim 1 comprising the amino acid sequence RLQALETLIQNQQRLNLWGSKGKLIS.

13. A diagnostic kit for detecting an antibody against a virus that causes immune deficiency comprising the peptide of claim 1.

14. The kit of claim 13 further comprising at least one control antibody which has a known binding affinity for said peptide.

15. The kit of claim 14 further comprising written instructions for using said kit.

16. A diagnostic composition for detecting in a sample an antibody against a retrovirus that causes immune deficiency, the diagnostic composition comprising the peptide of claim 1 and a detectable label.

17. The diagnostic composition of claim 16, wherein said peptide is detectably labeled.

18. A method of detecting in a sample an antibody against a retrovirus that causes immune deficiency, the method comprising contacting said sample with the diagnostic composition according to claim 16, and detecting the presence of antibody bound to said diagnostic agent as a result of said contacting.

19. An immunogen comprising (a) an amount of the peptide of claim 1 and (b) a physiologically-acceptable excipient therefor, wherein said amount is sufficient to elicit an immune response that protects a susceptible mammal against retrovirus infection.

20. A method for the immunization of a mammal against retrovirus infection, comprising administering to said mammal an effective amount of the immunogen of claim 19.

21. An isolated DNA molecule which encodes the peptide of claim 1.

22. A method of detecting in a sample nucleic acids encoding a retrovirus that causes immune deficiency, comprising the steps of: (a) hybridizing a labeled DNA molecule to nucleic acids encoding a retrovirus in said sample, wherein said labeled DNA molecule is prepared by labeling the DNA molecule according to claim 21 with a detectable label, and (b) detecting the hybridizing by means of said detectable label.

23. A method of detecting in a sample nucleic acids encoding a retrovirus that causes immune deficiency, comprising subjecting said nucleic acids to a Polymer Chain Reaction (PCR), wherein said PCR employs at least two oligonucleotide primers that anneal to a nucleic acid encoding a retrovirus that causes immune deficiency, wherein one of said primers is complementary to a first nucleotide sequence comprising the sequence of the DNA molecule according to claim 21, or its complementary sequence, wherein the other primer is complementary to a second nucleotide sequence comprising a nucleic acid molecule encoding a retrovirus that causes immune deficiency, whereby a geometrically amplified product is obtained only when said first and second nucleotide sequences occur within the same nucleic acid molecule encoding a retrovirus that causes immune deficiency.

L1 ANSWER 4 OF 13 USPATFULL on STN
2001:119046 METHOD OF DETECTING NUCLEIC ACID ENCODING A RETROVIRUS USING POLYMERASE CHAIN REACTION (PCR).
BRUST, STEFAN, MARBURG-MICHELBACH, Germany, Federal Republic of
KNAPP, STEFAN, MARGBURG, Germany, Federal Republic of
GERKEN, MANFRED, MARBURG, Germany, Federal Republic of
GUERTLER, LUTZ G., MUENCHEN, Germany, Federal Republic of
US 2001009667 A1 20010726
APPLICATION: US 1998-131551 A1 19980810 (9)
PRIORITY: DE 1994-4405810 19940223
DOCUMENT TYPE: Utility; APPLICATION.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Immunologically active peptides which are derived from a novel

immunodeficiency virus which has the designation MVP5180/91 are described. A diagnostic composition containing such a peptide and methods of detecting an antibody against a retrovirus that causes immune deficiency using such diagnostic composition are also described. A kit containing the immunologically active peptides is also described. An immunogen and method of immunizing a mammal against HIV infection using the immunologically active peptides is described. DNA encoding the peptides and methods of detecting nucleic acids encoding HIV viruses are also described.

CLM What is claimed is:

1. An immunologically active peptide comprising at least 15 consecutive amino acids selected from the amino acids in the following sequence: VWGIRQLRARLQALETLIQNQQRLNLWGXKGKLIXYTSVKWNTSWSGR, wherein X is C or S.

2. The peptide of claim 1, wherein said at least 15 consecutive amino acids are selected from the amino acids in the following amino acid sequence: RLQALETLIQNQQRLNLWGXKGKLIXYTSVKWN wherein X is C or S.

3. The peptide of claim 1 which binds antibodies against retroviruses of the HIV type.

4. The peptide of claim 1 comprising from 20 to 30 consecutive amino acids.

5. The peptide of claim 1 which further comprises, at one or both ends of the peptide, one or more sequences of amino acids, wherein said sequences are not taken from the amino acid sequence of the retrovirus MVP5180/91.

6. The peptide of claim 1, wherein X is C.

7. The peptide of claim 6, wherein C represents a cysteine residue in an oxidized state.

8. The peptide of claim 6 comprising the amino acid sequence RLQALETLIQNQQRLNLWGCKGKLIC.

9. The peptide of 8, wherein C represents a cysteine residue in an oxidized state.

10. The peptide of claim 6 comprising the amino acid sequence NQQRLNLWGCKGKLICYTSVKNW.

11. The peptide of claim 10, wherein C represents a cysteine residue in an oxidized state.

12. The peptide of claim 1 comprising the amino acid sequence RLQALETLIQNQQRLNLWGSKGKLIS.

13. A diagnostic kit for detecting an antibody against a virus that causes immune deficiency comprising the peptide of claim 1.

14. The kit of claim 13 further comprising at least one control antibody which has a known binding affinity for said peptide.

15. The kit of claim 14 further comprising written instructions for using said kit.

16. A diagnostic composition for detecting in a sample an antibody against a retrovirus that causes immune deficiency, the diagnostic composition comprising the peptide of claim 1 and a detectable label.

17. The diagnostic composition of claim 16, wherein said peptide is detectably labeled.

18. A method of detecting in a sample an antibody against a retrovirus

that causes immune deficiency, the method comprising contacting said sample with the diagnostic composition according to claim 16, and detecting the presence of antibody bound to said diagnostic agent as a result of said contacting.

19. An immunogen comprising (a) an amount of the peptide of claim 1 and (b) a physiologically-acceptable excipient therefor, wherein said amount is sufficient to elicit an immune response that protects a susceptible mammal against retrovirus infection.

20. A method for the immunization of a mammal against retrovirus infection, comprising administering to said mammal an effective amount of the immunogen of claim 19.

21. An isolated DNA molecule which encodes the peptide of claim 1.

22. A method of detecting in a sample nucleic acids encoding a retrovirus that causes immune deficiency, comprising the steps of: (a) hybridizing a labeled DNA molecule to nucleic acids encoding a retrovirus in said sample, wherein said labeled DNA molecule is prepared by labeling the DNA molecule according to claim 21 with a detectable label, and (b) detecting the hybridizing by means of said detectable label.

23. A method of detecting in a sample nucleic acids encoding a retrovirus that causes immune deficiency, comprising subjecting said nucleic acids to a Polymer Chain Reaction (PCR), wherein said PCR employs at least two oligonucleotide primers that anneal to a nucleic acid encoding a retrovirus that causes immune deficiency, wherein one of said primers is complementary to a first nucleotide sequence comprising the sequence of the DNA molecule according to claim 21, or its complementary sequence, wherein the other primer is complementary to a second nucleotide sequence comprising a nucleic acid molecule encoding a retrovirus that causes immune deficiency, whereby a geometrically amplified product is obtained only when said first and second nucleotide sequences occur within the same nucleic acid molecule encoding a retrovirus that causes immune deficiency.

L1 ANSWER 5 OF 13 USPATFULL on STN

2000:170857 Retrovirus from the HIV group and its use (MVP-2901/94).

Hauser, Hans-Peter, Marburg, Germany, Federal Republic of
Knapp, Stefan, Marburg, Germany, Federal Republic of
Brust, Stefan, Marburg, Germany, Federal Republic of
Gurtler, Lutz G., Munich, Germany, Federal Republic of
Eberle, Josef, Freising, Germany, Federal Republic of
Kaptue, Lazare, Yaounde/Cameroun, Germany, Federal Republic of
Zekeng, Leopold Achengui, Yaounde/Cameroun, Germany, Federal Republic of
Behringwerke Aktiengesellschaft, Marburg, Germany, Federal Republic of (non-U.S. corporation)

US 6162631 20001219

APPLICATION: US 1997-989493 19971212 (8)

PRIORITY: DE 1995-19505262 19950216

DOCUMENT TYPE: Utility; Granted.

AB A novel immunodeficiency virus is disclosed which has the designation MVP-2901/94 and which has been deposited with the European Collection of Animal Cell Cultures (ECACC) under No. V 95012601. The characteristic antigens which can be obtained from the virus and which can be employed for detecting antibodies against retroviruses which are associated with immunodeficiency diseases are also disclosed, as are the partial DNA and amino acid sequences of the virus.

CLM What is claimed is:

1. An isolated virus which binds with antibodies to a polypeptide wherein said polypeptide consists of the amino acid sequence at positions 319-341 in SEQ ID NO: 12.

2. The isolated virus of claim 1, wherein said virus is a retrovirus, the genome of which consists of a nucleotide sequence which is at least 85% identical to the nucleotide sequence of the genome of retrovirus MVP 2901/94 which has been deposited with the European Collection of Animal Cell Culture (ECACC) under No. 95012601 and wherein said isolated virus has all the morphological and immunological properties of retrovirus MVP-2901/94.

3. The isolated retrovirus of claim 2, the genome of which consists of a nucleotide sequence which is at least 90% identical to the nucleotide sequence to the genome of retrovirus MVP-2901/94.

4. Isolated virus having the ECACC accession no. V 95012601.

5. An isolated polypeptide consisting of an amino acid sequence set forth in SEQ ID NO: 12.

6. An isolated virus having all the identifying characteristics of the virus designated MVP 2901/94 having ECACC Accession No. 95012601.

L1 ANSWER 11 OF 13 USPATFULL on STN
1998:134790 Peptides derived from a retrovirus of the HIV group and their use.
Brust, Stefan, Marburg-Michelbach, Germany, Federal Republic of
Knapp, Stefan, Marburg, Germany, Federal Republic of
Gerken, Manfred, Marburg, Germany, Federal Republic of
Guertler, Lutz G., Munich, Germany, Federal Republic of
Dade Behring Marburg GmbH, Marburg, Germany, Federal Republic of (non-U.S. corporation)
US 5830634 19981103
APPLICATION: US 1995-394021 19950223 (8)
PRIORITY: DE 1994-4405810 19940223
DOCUMENT TYPE: Utility; Granted.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Immunologically active peptides which are derived from a novel immunodeficiency virus which has the designation MVP5180/91 are described. A diagnostic composition containing such a peptide and methods of detecting an antibody against a retrovirus that causes immune deficiency using such diagnostic composition are also described. A kit containing the immunologically active peptides is also described. An immunogen and method of immunizing a mammal against HIV infection using the immunologically active peptides is described. DNA encoding the peptides and methods of detecting nucleic acids encoding HIV viruses are also described.
CLM What is claimed is:
1. A peptide consisting of the following amino acid sequence: VWGIRQLRARLQALETLIQNQQRLNLWGXKGKLIXYTSVKWNTSWSGR (SEQ ID NO:1), wherein X is C.

2. The peptide of claim 1, wherein C represents a cysteine residue in an oxidized state.

3. A peptide consisting of the following amino acid sequence: VWGIRQLRARLQALETLIQNQQRLNLWGXKGKLIXYTSVKWNTSWSGR (SEQ ID NO:1), wherein X is S.

4. A peptide consisting of the following amino acid sequence: RLQALETLIQNQQRLNLWGXKGKLIXYTSVKWN (residues 10-42 of SEQ ID NO:1), wherein X is S.

5. A peptide consisting of the following amino acid sequence: NQQRLNLWGCKGKLICYTSVKWN (SEQ ID NO:2).

6. The peptide of claim 5, wherein C represents a cysteine residue in an oxidized state.

7. A peptide consisting of the following amino acid sequence: RLQALETLIQNQQRLNLWGCKGKLIC (SEQ ID NO:3).

8. The peptide of claim 7, wherein C represents a cysteine residue in an oxidized state.

9. A peptide consisting of the following amino acid sequence: RLQALETLIQNQQRLNLWGSKGKLIS (SEQ ID NO:4).

10. A peptide comprising: at least 15 consecutive amino acid residues selected from the following sequence: VWGIRQLRARLQALETLIQNQQRLNLWGXKGKLI XYTSVKWNTSWSGR (SEQ ID NO:1), wherein X is C or S, and at one or both ends of the 15 consecutive amino acid residues, one or more sequences of amino acids, wherein the sequences are not taken from the amino acid sequence of the retrovirus MVP5180/91.

11. The peptide of claim 10, wherein the sequences not taken from the amino acid sequence of the retrovirus MVP5180/91 are from a human immune deficiency virus other than the retrovirus MVP5180/91.

12. The peptide of claim 10, wherein the sequences not taken from the amino acid sequence of the retrovirus MVP5180/91 are from a human immune deficiency virus selected from the group consisting of HIV-1, HIV-2 and HIV-3.

13. A peptide comprising: the following amino acid sequence: VWGIRQLRARLQALETLIQNQQRLNLWGXKGKLIXYTSVKWNTSWSGR (SEQ ID NO:1), wherein X is C, and at one or both ends of the amino acid sequence, one or more sequences of amino acids from a human immune deficiency virus selected from the group consisting of HIV-1, HIV-2 and HIV-3.

14. A peptide comprising: the following amino acid sequence: VWGIRQLRARLQALETLIQNQQRLNLWGXKGKLIXYTSVKWNTSWSGR (SEQ ID NO:1), wherein X is S, and at one or both ends of the amino acid sequence, one or more sequences of amino acids from a human immune deficiency virus selected from the group consisting of HIV-1, HIV-2 and HIV-3.

15. A peptide comprising: the following amino acid sequence: RLQALETLIQNQQRLNLWGXKGKLIXYTSVKWN (residues 10-42 of SEQ ID NO:1), wherein X is S, and at one or both ends of the amino acid sequence, one or more sequences of amino acids from a human immune deficiency virus selected from the group consisting of HIV-1, HIV-2 and HIV-3.

16. A peptide comprising: the following amino acid sequence: NQQRLNLWGCKGKLICYTSVKWN (SEQ ID NO:2), and at one or both ends of the amino acid sequence, one or more sequences of amino acids from a human immune deficiency virus selected from the group consisting of HIV-1, HIV-2 and HIV-3.

17. A peptide comprising: the following amino acid sequence: RLQALETLIQNQQRLNLWGCKGKLIC (SEQ ID NO:3), and at one or both ends of the amino acid sequence, one or more sequences of amino acids from a human immune deficiency virus selected from the group consisting of HIV-1, HIV-2 and HIV-3.

18. A peptide comprising: the following amino acid sequence: RLQALETLIQNQQRLNLWGSKGKLIS (SEQ ID NO:4), and at one or both ends of the amino acid sequence, one or more sequences of amino acids from a human immune deficiency virus selected from the group consisting of HIV-1, HIV-2 and HIV-3.

19. A diagnostic kit for detecting an antibody against an HIV-1 subtype O virus, comprising a peptide consisting of the following amino acid sequence: VWGIRQLRARLQALETLIQNQQRLNLWGXKGKLIXYTSVKWNTSWSGR (SEQ ID NO:1), wherein X is C, and at least one control antibody which has a known binding affinity for the peptide.

20. A diagnostic kit for detecting an antibody against an HIV-1 subtype O virus, comprising a peptide consisting of the following amino acid sequence: VWGIRQLRARLQALETLIQNQQRLNLWGXKGKLIXYTSVKWNTSWSGR (SEQ ID NO:1), wherein X is S, and at least one control antibody which has a known binding affinity for the peptide.

21. A diagnostic kit for detecting an antibody against an HIV-1 subtype O virus, comprising a peptide consisting of the following amino acid sequence: RLQALETLIQNQQRLNLWGXKGKLIXYTSVKWN (residues 10-42 of SEQ ID NO:1), wherein X is S, and at least one control antibody which has a known binding affinity for the peptide.

22. A diagnostic kit for detecting an antibody against an HIV-1 subtype O virus, comprising a peptide consisting of the following amino acid sequence: NQQRLNLWGCKGKLICYTSVKWN (SEQ ID NO:2), and at least one control antibody which has a known binding affinity for the peptide.

23. A diagnostic kit for detecting an antibody against an HIV-1 subtype O virus, comprising a peptide consisting of the following amino acid sequence: RLQALETLIQNQQRLNLWGCKGKLIC (SEQ ID NO:3), and at least one control antibody which has a known binding affinity for the peptide.

24. A diagnostic kit for detecting an antibody against an HIV-1 subtype O virus, comprising a peptide consisting of the following amino acid sequence: RLQALETLIQNQQRLNLWGSKGKLIS (SEQ ID NO:4), and at least one control antibody which has a known binding affinity for the peptide.

25. A diagnostic kit for detecting an antibody against an HIV-1 subtype O virus, comprising a peptide comprising at least 15 consecutive amino acid residues selected from the following sequence: VWGIRQLRARLQALETLIQNQQRLNLWGXKGKLIXYTSVKWNTSWSGR (SEQ ID NO:1), wherein X is C or S, and, at one or both ends of the at least 15 consecutive amino acid residues, one or more sequences of amino acids, wherein the sequences are not taken from the amino acid sequence of the retrovirus MVP5180/91, and at least one control antibody which has a known binding affinity for the peptide.

26. A diagnostic composition for detecting in a sample an antibody against an HIV-1 subtype O virus, comprising a peptide consisting of the following amino acid sequence: VWGIRQLRARLQALETLIQNQQRLNLWGXKGKLIXYTSVKW NTSWSGR (SEQ ID NO:1), wherein X is C, and a detectable label.

27. A diagnostic composition for detecting in a sample an antibody against an HIV-1 subtype O virus, comprising a peptide consisting of the following amino acid sequence: VWGIRQLRARLQALETLIQNQQRLNLWGXKGKLIXYTSVKW NTSWSGR (SEQ ID NO:1), wherein X is S, and a detectable label.

28. A diagnostic composition for detecting in a sample an antibody against an HIV-1 subtype O virus, comprising a peptide consisting of the following amino acid sequence: RLQALETLIQNQQRLNLWGXKGKLIXYTSVKWN (residues 10-42 of SEQ ID NO:1), wherein X is S, and a detectable label.

29. A diagnostic composition for detecting in a sample an antibody against an HIV-1 subtype O virus, comprising a peptide consisting of the following amino acid sequence: NQQRLNLWGCKGKLICYTSVKWN (SEQ ID NO:2), and a detectable label.

30. A diagnostic composition for detecting in a sample an antibody against an HIV-1 subtype O virus, comprising a peptide consisting of the following amino acid sequence: RLQALETLIQNQQRLNLWGCKGKLIC (SEQ ID NO:3), and a detectable label.

31. A diagnostic composition for detecting in a sample an antibody against an HIV-1 subtype O virus, comprising a peptide consisting of the following amino acid sequence: RLQALETLIQNQQRLNLWGSKGKLIS (SEQ ID NO:4),

and a detectable label.

32. A diagnostic composition for detecting in a sample an antibody against an HIV-1 subtype O virus, comprising a peptide comprising at least 15 consecutive amino acid residues selected from the following sequence: VWGIRQLRARLQALETLIQNQQRLNLWGXKGKLIXYTSVKWNTSWSGR (SEQ ID NO:1), wherein X is C or S, and, at one or both ends of the at least 15 consecutive amino acid residues, one or more sequences of amino acids, wherein the sequences are not taken from the amino acid sequence of the retrovirus MVP5180/91, and a detectable label.

33. A method of detecting in a sample an antibody against an HIV-1 subtype O virus, comprising contacting the sample with a diagnostic composition comprising a peptide consisting of the following amino acid sequence: VWGIRQLRARLQALETLIQNQQRLNLWGXKGKLIXYTSVKWNTSWSGR (SEQ ID NO:1), wherein X is C, and a detectable label, and detecting the presence of antibody bound to the diagnostic agent as a result of the contacting.

34. A method of detecting in a sample an antibody against an HIV-1 subtype O virus, comprising contacting the sample with a diagnostic composition comprising a peptide consisting of the following amino acid sequence: VWGIRQLRARLQALETLIQNQQRLNLWGXKGKLIXYTSVKWNTSWSGR (SEQ ID NO:1), wherein X is S, and a detectable label, and detecting the presence of antibody bound to the diagnostic agent as a result of the contacting.

35. A method of detecting in a sample an antibody against an HIV-1 subtype O virus, comprising contacting the sample with a diagnostic composition comprising a peptide consisting of the following amino acid sequence: RLQALETLIQNQQRLNLWGXKGKLIXYTSVKWN (residues 10-42 of SEQ ID NO:1), wherein X is S and a detectable label, and detecting the presence of antibody bound to the diagnostic agent as a result of the contacting.

36. A method of detecting in a sample an antibody against an HIV-1 subtype O virus, comprising contacting the sample with a diagnostic composition comprising a peptide consisting of the following amino acid sequence: NQQRLNLWGCKGKLICYTSVKWN (SEQ ID NO:2), and a detectable label, and detecting the presence of antibody bound to the diagnostic agent as a result of the contacting.

37. A method of detecting in a sample an antibody against an HIV-1 subtype O virus, comprising contacting the sample with a diagnostic composition comprising a peptide consisting of the following amino acid sequence: RLQALETLIQNQQRLNLWGCKGKLIC (SEQ ID NO:3) and a detectable label, and detecting the presence of antibody bound to the diagnostic agent as a result of the contacting.

38. A method of detecting in a sample an antibody against an HIV-1 subtype O virus, comprising contacting the sample with a diagnostic composition comprising a peptide consisting of the following amino acid sequence: RLQALETLIQNQQRLNLWGSKGKLIS (SEQ ID NO:4), and a detectable label, and detecting the presence of antibody bound to the diagnostic agent as a result of the contacting.

39. A method of detecting in a sample an antibody against an HIV-1 subtype O virus, comprising contacting the sample with a diagnostic composition comprising a detectable label and a peptide comprising at least 15 consecutive amino acid residues selected from the following sequence: VWGIRQLRARLQALETLIQNQQRLNLWGXKGKLIXYTSVKWNTSWSGR (SEQ ID NO:1), wherein X is C or S, and, at one or both ends of the at least 15 consecutive amino acid residues, one or more sequences of amino acids, wherein the sequences are not taken from the amino acid sequence of the retrovirus MVP5180/91, and detecting the presence of antibody bound to the diagnostic agent as a result of the contacting.

L1 ANSWER 12 OF 13 USPATFULL on STN
1998:101498 Retrovirus from the HIV type O and its use (MVP-2901/94).
Hauser, Hans-Peter, Marburg, Germany, Federal Republic of
Knapp, Stefan, Marburg, Germany, Federal Republic of
Brust, Stefan, Marburg, Germany, Federal Republic of
Gurtler, Lutz G., Munich, Germany, Federal Republic of
Eberle, Josef, Freising, Germany, Federal Republic of
Kaptue, Lazare, Yaounde/Cameroun, Germany, Federal Republic of
Zekeng, Leopold Achenqui, Yaounde/Cameroun, Germany, Federal Republic of
Behringwerke Aktiengesellschaft, Marburg, Germany, Federal Republic of
(non-U.S. corporation)
US 5798205 19980825
APPLICATION: US 1996-602713 19960216 (8)
PRIORITY: DE 1995-19505262 19950216
DOCUMENT TYPE: Utility; Granted.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB A novel HIV type O immunodeficiency virus is disclosed which has the designation MVP-2901/94 and which has been deposited with the European Collection of Animal Cell Cultures (ECACC) under No. V 95012601. The characteristic antigens which can be obtained from the virus and which can be employed for detecting antibodies against retroviruses which are associated with immunodeficiency diseases are also disclosed, as are the partial DNA and amino acid sequences of the virus.

CLM What is claimed is:

1. An isolated protein, polypeptide or peptide which comprises at least 10 contiguous amino acids found at positions 319-341 of the amino acid sequence set forth in SEQ ID NO: 12.

2. The isolated protein, polypeptide or peptide of claim 1, comprising at least 20 continuous amino acids found at positions 319-341 of the amino acid sequence set forth in SEQ ID NO: 12.

3. A method for detecting an antibody which binds with human immunodeficiency virus MVP 2901/94 in a sample comprising contacting said sample with the protein, polypeptide or peptide of claim 5 and determining binding of any antibody in said sample to said protein, polypeptide or peptide as a determination of said virus in said sample.

4. The method of claim 3, further comprising contacting said sample with an antibody which binds to said antibodies, and determining binding therebetween.

5. The isolated protein, polypeptide or peptide of claim 2, wherein said protein, polypeptide or peptide binds with antibodies produced against retrovirus MVP 2901/94.

6. A test kit for detecting presence of an antibody which binds with human immunodeficiency virus MVP 2901/94 in a sample, comprising the isolated protein, polypeptide or peptide of 5, and a substance which specifically binds to an antibody which binds to said virus.

7. The test kit of claim 6, wherein said substance is protein A.

8. The test kit of claim 6, wherein said substance is an antibody.

9. The isolated protein, polypeptide or peptide of claim 1, wherein said protein, polypeptide or peptide binds with antibodies produced against retrovirus MVP 2901/94.

10. A method for detecting an antibody which binds with human immunodeficiency virus MVP 2901/94 in a sample, comprising contacting said sample with the isolated protein, polypeptide or peptide of claim 9 and determining binding of any antibody in said sample to said protein, polypeptide or peptide as a determination of said virus in said sample.

11. The method of claim 10, further comprising contacting said sample with a second antibody which binds to said antibody.

12. A test kit for detecting an antibody which binds with human immunodeficiency virus MVP 2901/94 in a sample, comprising the isolated protein, polypeptide or peptide of claim 9, and a substance which specifically binds to an antibody which binds to said virus.

13. The test kit of claim 12, wherein said substance is protein A.

14. The test kit of claim 12, wherein said substance is an antibody.

15. The test kit of claim 14, wherein said antibody is labelled with an enzyme or a fluorescent molecule.

16. The test kit of claim 12, wherein said substance is labelled with an enzyme or a fluorescent molecule.

17. The isolated protein, polypeptide or peptide of claim 1, consisting of amino acids 319-341 of SEQ ID NO: 12, with the proviso that the fourth amino acid is Arg, rather than Leu.

18. A method for detecting an antibody which binds with human immunodeficiency virus MVP 2901/94 in a sample, comprising contacting said sample with the isolated polypeptide of claim 7, and determining binding of antibodies in said sample to said polypeptide as a determination of virus in said sample.

19. A test kit for detecting presence of an antibody which binds with human immunodeficiency virus MVP 2901/94 in a sample, comprising the isolated polypeptide of claim 17, and a substance which specifically binds to an antibody which binds to said virus.

20. The test kit of claim 19, wherein said substance is protein A.

21. The test kit of claim 19, wherein said substance is an antibody.

22. The test kit of claim 19, wherein said substance is labelled with an enzyme or a fluorescent molecule.

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=> s 6335158/pn
L2            0 6335158/PN

=> s us6335158/pn
L3            1 US6335158/PN

=> d l3,cbib,ab,clm

L3   ANSWER 1 OF 1  USPATFULL on STN
2001:119046 METHOD OF DETECTING NUCLEIC ACID ENCODING A RETROVIRUS USING
    POLYMERASE CHAIN REACTION (PCR).
    BRUST, STEFAN, MARBURG-MICHELBACH, Germany, Federal Republic of
    KNAPP, STEFAN, MARGBURG, Germany, Federal Republic of
    GERKEN, MANFRED, MARBURG, Germany, Federal Republic of
    GUERTLER, LUTZ G., MUENCHEN, Germany, Federal Republic of
    US 2001009667 A1 20010726
    APPLICATION: US 1998-131551  A1  19980810 (9)
    PRIORITY: DE 1994-4405810  19940223
    DOCUMENT TYPE: Utility; APPLICATION.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB      Immunologically active peptides which are derived from a novel
        immunodeficiency virus which has the designation MVP5180/91 are
        described. A diagnostic composition containing such a peptide and
        methods of detecting an antibody against a retrovirus that causes immune
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deficiency using such diagnostic composition are also described. A kit containing the immunologically active peptides is also described. An immunogen and method of immunizing a mammal against HIV infection using the immunologically active peptides is described. DNA encoding the peptides and methods of detecting nucleic acids encoding HIV viruses are also described.

CLM What is claimed is:

1. An immunologically active peptide comprising at least 15 consecutive amino acids selected from the amino acids in the following sequence: VWGIRQLRARLQALETLIQNQQRLNLWGXKGKLIXYTSVKWNTSWSGR, wherein X is C or S.

2. The peptide of claim 1, wherein said at least 15 consecutive amino acids are selected from the amino acids in the following amino acid sequence: RLQALETLIQNQQRLNLWGXKGKLIXYTSVKWN wherein X is C or S.

3. The peptide of claim 1 which binds antibodies against retroviruses of the HIV type.

4. The peptide of claim 1 comprising from 20 to 30 consecutive amino acids.

5. The peptide of claim 1 which further comprises, at one or both ends of the peptide, one or more sequences of amino acids, wherein said sequences are not taken from the amino acid sequence of the retrovirus MVP5180/91.

6. The peptide of claim 1, wherein X is C.

7. The peptide of claim 6, wherein C represents a cysteine residue in an oxidized state.

8. The peptide of claim 6 comprising the amino acid sequence RLQALETLIQNQQRLNLWGCKGKLIC.

9. The peptide of 8, wherein C represents a cysteine residue in an oxidized state.

10. The peptide of claim 6 comprising the amino acid sequence NQQRLNLWGCKGKLICYTSVKNW.

11. The peptide of claim 10, wherein C represents a cysteine residue in an oxidized state.

12. The peptide of claim 1 comprising the amino acid sequence RLQALETLIQNQQRLNLWGSKGKLIS.

13. A diagnostic kit for detecting an antibody against a virus that causes immune deficiency comprising the peptide of claim 1.

14. The kit of claim 13 further comprising at least one control antibody which has a known binding affinity for said peptide.

15. The kit of claim 14 further comprising written instructions for using said kit.

16. A diagnostic composition for detecting in a sample an antibody against a retrovirus that causes immune deficiency, the diagnostic composition comprising the peptide of claim 1 and a detectable label.

17. The diagnostic composition of claim 16, wherein said peptide is detectably labeled.

18. A method of detecting in a sample an antibody against a retrovirus that causes immune deficiency, the method comprising contacting said sample with the diagnostic composition according to claim 16, and detecting the presence of antibody bound to said diagnostic agent as a

result of said contacting.

19. An immunogen comprising (a) an amount of the peptide of claim 1 and (b) a physiologically-acceptable excipient therefor, wherein said amount is sufficient to elicit an immune response that protects a susceptible mammal against retrovirus infection.

20. A method for the immunization of a mammal against retrovirus infection, comprising administering to said mammal an effective amount of the immunogen of claim 19.

21. An isolated DNA molecule which encodes the peptide of claim 1.

22. A method of detecting in a sample nucleic acids encoding a retrovirus that causes immune deficiency, comprising the steps of: (a) hybridizing a labeled DNA molecule to nucleic acids encoding a retrovirus in said sample, wherein said labeled DNA molecule is prepared by labeling the DNA molecule according to claim 21 with a detectable label, and (b) detecting the hybridizing by means of said detectable label.

23. A method of detecting in a sample nucleic acids encoding a retrovirus that causes immune deficiency, comprising subjecting said nucleic acids to a Polymer Chain Reaction (PCR), wherein said PCR employs at least two oligonucleotide primers that anneal to a nucleic acid encoding a retrovirus that causes immune deficiency, wherein one of said primers is complementary to a first nucleotide sequence comprising the sequence of the DNA molecule according to claim 21, or its complementary sequence, wherein the other primer is complementary to a second nucleotide sequence comprising a nucleic acid molecule encoding a retrovirus that causes immune deficiency, whereby a geometrically amplified product is obtained only when said first and second nucleotide sequences occur within the same nucleic acid molecule encoding a retrovirus that causes immune deficiency.

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=> d his

     (FILE 'HOME' ENTERED AT 20:50:07 ON 19 FEB 2004)

     FILE 'USPATFULL' ENTERED AT 20:50:23 ON 19 FEB 2004

     FILE 'USPATFULL' ENTERED AT 20:50:50 ON 19 FEB 2004
                E BRUST STEFAN/IN
L1             13 S E3
L2              0 S 6335158/PN
L3              1 S US6335158/PN

=> e knapp stefan/in
E1              1     KNAPP SIEGBERT/IN
E2              1     KNAPP SR GENE P/IN
E3             24 --> KNAPP STEFAN/IN
E4              1     KNAPP STEPHEN E/IN
E5              3     KNAPP STEPHEN L/IN
E6              2     KNAPP STEVEN E/IN
E7              7     KNAPP STEVEN K/IN
E8              1     KNAPP SUZANNE C/IN
E9              1     KNAPP TAMMY W/IN
E10            13     KNAPP TERRY R/IN
E11             1     KNAPP TERRY RUSSELL/IN
E12             1     KNAPP THEODORE L/IN

=> s e3
L4             24 "KNAPP STEFAN"/IN
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=> s l4 not l1
L5          16 L4 NOT L1

=> d l5,ti,1-5

L5   ANSWER 1 OF 16  USPATFULL on STN
TI     Retrovirus from the HIV group and its use

L5   ANSWER 2 OF 16  USPATFULL on STN
TI     Retrovirus from the HIV group and its use

L5   ANSWER 3 OF 16  USPATFULL on STN
TI     Retrovirus from the HIV group and its use

L5   ANSWER 4 OF 16  USPATFULL on STN
TI     Retrovirus from the HIV group and its use

L5   ANSWER 5 OF 16  USPATFULL on STN
TI     Retrovirus from the HIV group and its use


=> d l5,ti,1-16

L5   ANSWER 1 OF 16  USPATFULL on STN
TI     Retrovirus from the HIV group and its use

L5   ANSWER 2 OF 16  USPATFULL on STN
TI     Retrovirus from the HIV group and its use

L5   ANSWER 3 OF 16  USPATFULL on STN
TI     Retrovirus from the HIV group and its use

L5   ANSWER 4 OF 16  USPATFULL on STN
TI     Retrovirus from the HIV group and its use

L5   ANSWER 5 OF 16  USPATFULL on STN
TI     Retrovirus from the HIV group and its use

L5   ANSWER 6 OF 16  USPATFULL on STN
TI     Toxoplasma gondii antigens, the preparation thereof and the use thereof

L5   ANSWER 7 OF 16  USPATFULL on STN
TI     Toxoplasma gondii antigens, the preparation thereof and the use thereof

L5   ANSWER 8 OF 16  USPATFULL on STN
TI     Diagnostic assay for detection of HIV

L5   ANSWER 9 OF 16  USPATFULL on STN
TI     Toxoplasma gondii antigens, the preparation thereof and the use thereof

L5   ANSWER 10 OF 16  USPATFULL on STN
TI     Retrovirus from the HIV group and its use

L5   ANSWER 11 OF 16  USPATFULL on STN
TI     Retrovirus from the HIV group and its use

L5   ANSWER 12 OF 16  USPATFULL on STN
TI     Retrovirus from the HIV group and its use

L5   ANSWER 13 OF 16  USPATFULL on STN
TI     Nucleic acid encoding a signal peptide, a recombinant molecule
       comprising the nucleic acid, methods of using the nucleic acid, and
       methods of using the signal peptide

L5   ANSWER 14 OF 16  USPATFULL on STN
TI     Electromagnetically actuated valve
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L5 ANSWER 15 OF 16 USPATFULL on STN
TI Device for feeding vapors of a fuel tank into an internal combustion engine

L5 ANSWER 16 OF 16 USPATFULL on STN
TI Signal peptide for the secretion of peptides in Escherichia coli

> d l5,cbib,ab,clm,1-16

5 ANSWER 1 OF 16 USPATFULL on STN
003:238757 Retrovirus from the HIV group and its use.
Guertler, Lutz G., Muenchen, GERMANY, FEDERAL REPUBLIC OF
Eberle, Josef, Freising, GERMANY, FEDERAL REPUBLIC OF
Brunn, Albrecht V., Augsburg, GERMANY, FEDERAL REPUBLIC OF
Knapp, Stefan, Marburg-Wehrshausen, GERMANY, FEDERAL REPUBLIC OF
Hauser, Hans-Peter, Marburg, GERMANY, FEDERAL REPUBLIC OF
US 2003166915 A1 20030904
APPLICATION: US 2002-326090 A1 20021223 (10)
PRIORITY: DE 1992-4233646 19921006
DE 1992-4235718 19921022
DE 1992-4244541 19921230
DE 1993-4318186 19930601
DOCUMENT TYPE: Utility; APPLICATION.
AS INDEXING IS AVAILABLE FOR THIS PATENT.
B A novel immunodeficiency virus is disclosed which has the designation MVP-5180/91 and which has been deposited with the European Collection of Animal Cell Cultures (ECACC) under No. V 920 52 318. The characteristic antigens which can be obtained from it and which can be employed for detecting antibodies against retroviruses which are associated with immunodeficiency diseases are also disclosed, as are the DNA and amino acid sequences of the virus.
LM What is claimed is:
1) an immunodeficiency virus of the HIV group, or variants of this virus, which exhibits the essential morphological and immunological properties of the retrovirus which has the designation MVP-5180/91 and which has been deposited with the European collection of animal cell cultures (ECACC) under no: V 920 92 318.

2) The immunodeficiency virus as claimed in claim 1, which exhibits a protein band in a Western blot which corresponds to reverse transcriptase and is 3-7 kilodaltons smaller than the corresponding band of the HIV-1 and/or HIV-2 viruses.

3) The immunodeficiency virus as claimed in one of claims 1 or 2, which retrovirus exhibits less reactivity with a monoclonal antibody directed against protein p 24, related to reverse transcriptase activity, than does the HIV-1 virus, and more activity, related to the activity of reverse transcriptase, than does HIV-2.

4) The immunodeficiency virus as claimed in one of the preceding claims, wherein antigen/antibody reactions with its transmembrane protein gp 41 are readily detectable using sera from patients originating from Africa, and wherein only a relatively small antigen/antibody reaction, or no such reaction, can be detected with the gp-41 using sera from patients originating from Germany.

5) The immunodeficiency virus as claimed in one of the abovementioned claims, which has an RNA sequence which is homologous to the extent of about 75% or more, based on the entire genome, with the RNA of the deposited virus.

6) The immunodeficiency virus as claimed in one of the abovementioned claims, which has an RNA sequence which is homologous to the extent of at least 75% with the RNA sequence of Table 1.

7) The immunodeficiency virus as claimed in one of claims 1 to 5, which has a nucleotide sequence which is homologous to the extent of at least 75% with the sequence of Table 3, or parts thereof.

8) The immunodeficiency virus as claimed in claim 7, wherein the part of the sequence is at least 50 nucleotides long.

9) The immunodeficiency virus as claimed in one of the preceding claims, which has a sequence or constituent sequence which corresponds to FIG. 4 or is homologous to this sequence, where the differences from the sequence given in FIG. 4, related to the gene loci, are at most: LTR: 17%, GAG: 29%, POL: 25%, VIF: 31%, ENV: 46%, NEF: 16%.

10) The immunodeficiency virus as claimed in one of the preceding claims, which has a sequence or constituent sequence which corresponds to FIG. 4 or is homologous to this sequence, where the differences from the sequence given in FIG. 4, related to the gene loci, are at most: LTR: 10%, GAG: 14%, POL: 12%, VIF: 15%, ENV: 22%, NEF: 10%.

11) cDNA which is complementary to the RNA, or parts thereof, of the immunodeficiency virus MVP-5180/91 deposited with the European Collection of Animal Cell Cultures (ECACC) under No. V 920 92 318, or of a virus as claimed in one of claims 1-10.

12) Recombinant DNA which contains cDNA as claimed in claim 11.

13) An antigen which was prepared using the cDNA as claimed in claim 11 or the recombinant DNA as claimed in claim 12, or using the amino acid structure which can be deduced from its cDNA.

14) The antigen as claimed in claim 13, which is a protein or peptide.

15) The antigen as claimed in one of claims 13 or 14, which has an amino acid sequence which corresponds to Table 3 or to a constituent sequence thereof.

16) The antigen as claimed in claim 15, wherein the constituent sequence has at least 10 amino acids.

17) The antigen as claimed in claim 15, which has the amino acid sequence RLQALETLIQNQQRLNLWGCKGKLICYTSVKWNTS, or a constituent sequence thereof having at least 6 consecutive amino acids.

18) An antigen which was prepared from an immunodeficiency virus as claimed in one of claims 1 to 10.

19) The antigen as claimed in one of claims 13 to 18, which was prepared recombinantly.

20) The antigen as claimed in one of claims 13 to 17, which was prepared synthetically.

21) A test kit for detecting antibodies against viruses which cause immuno deficiency, wherein antigen as claimed in claims 13 to 20 is employed.

22) The test kit as claimed in claim 21, which is a Western blot.

23) The test kit as claimed in claim 21, which is an ELISA test or a fluorescence-antibody detection test.

24) Use of the immunodeficiency virus as claimed in one of claims 1 to 10 and/or of the cDNA as claimed in claim 11 or 12 and/or of an antigen as claimed in claims 13 to 20 for detecting retroviruses which cause immune deficiency.

25) Use of a retrovirus as claimed in one of claims 1 to 10, of a cDNA as claimed in claim 11 or 12 and/or of an antigen as claimed in claims 13 to 20 for preparing vaccines.

26) Ribonucleic acid characterized in that the ribonucleic acid is coding for an immunodeficiency virus according to one of claims 1 to 10.

27. A nucleic acid comprising the sequence of the genome of virus MvP-5180/91 (SEQ ID NO: 56).

28. The nucleic acid of claim 27, wherein said nucleic acid is DNA.

29. The nucleic acid of claim 27, wherein said nucleic acid is RNA.

30. A nucleic acid comprising the sequence of SEQ ID NO: 38 or SEQ ID NO: 39.

31. A nucleic acid comprising the sequence of SEQ ID NO: 44 or SEQ ID NO: 45.

32. A nucleic acid comprising a nucleotide sequence having more than 66% homology with SEQ ID NO: 44 or SEQ ID NO: 45, over the length of SEQ ID NO: 44 or SEQ ID NO: 45, respectively.

33. The nucleic acid of claim 32, wherein said nucleic acid comprises a nucleotide sequence having more than 75% homology with SEQ ID NO: 44 or SEQ ID NO: 45, over the length of SEQ ID NO: 44 or SEQ ID NO: 45, respectively.

34. The nucleic acid of claim 33, wherein said nucleic acid comprises a nucleotide sequence having more than 85% homology with SEQ ID NO: 44 or SEQ ID NO: 45, over the length of SEQ ID NO: 44 or SEQ ID NO: 45, respectively.

35. A nucleic acid comprising a nucleotide sequence having more than 66% homology with SEQ ID NO: 37 or SEQ ID NO: 38, over the length of SEQ ID NO: 37 or SEQ ID NO: 38, respectively.

36. The nucleic acid of claim 35, wherein said nucleic acid comprises a nucleotide sequence having more than 75% homology with SEQ ID NO: 37 or SEQ ID NO: 38, over the length of SEQ ID NO: 37 or SEQ ID NO: 38, respectively.

37. The nucleic acid of claim 36, wherein said nucleic acid comprises a nucleotide sequence having more than 85% homology with SEQ ID NO: 37 or SEQ ID NO: 38, over the length of SEQ ID NO: 37 or SEQ ID NO: 38, respectively.

38. A nucleic acid comprising at least 50 consecutive nucleotides of SEQ ID NO: 56.

39. The nucleic acid of claim 38, said nucleic acid comprising at least 100 consecutive nucleotides of SEQ ID NO: 56.

L5 ANSWER 2 OF 16 USPATFULL on STN
2003:3408 Retrovirus from the HIV group and its use.
Guertler, Lutz G., Muenchen, GERMANY, FEDERAL REPUBLIC OF
Eberle, Josef, Freising, GERMANY, FEDERAL REPUBLIC OF
Brunn, Albrecht V., Augsburg, GERMANY, FEDERAL REPUBLIC OF
Knapp, Stefan, Marburg-Wehrshausen, GERMANY, FEDERAL REPUBLIC OF
Hauser, Hans-Peter, Marburg, GERMANY, FEDERAL REPUBLIC OF
Dade Behring Marburg GmbH (non-U.S. corporation)
US 2003003443 A1 20030102
APPLICATION: US 2001-886159 A1 20010622 (9)

PRIORITY: DE 1992-4233646 19921006
DE 1992-4235718 19921022
DE 1992-4244541 19921230
DE 1993-4318186 19930601
DOCUMENT TYPE: Utility; APPLICATION.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB A novel immunodeficiency virus is disclosed which has the designation MVP-5180/91 and which has been deposited with the European Collection of Animal Cell Cultures (ECACC) under No. V 920 52 318. The characteristic antigens which can be obtained from it and which can be employed for detecting antibodies against retroviruses which are associated with immunodeficiency diseases are also disclosed, as are the DNA and amino acid sequences of the virus.

CLM What is claimed is:

1. an immunodeficiency virus of the HIV group, or variants of this virus, which exhibits the essential morphological and immunological properties of the retrovirus which has the designation MVP-5180/91 and which has been deposited with the European Collection of Animal Cell Cultures (ECACC) under No V 920 92 318.

2. The immunodeficiency virus as claimed in claim 1, which exhibits a protein band in a Western blot which corresponds to reverse transcriptase and is 3-7 kilodaltons smaller than the corresponding band of the HIV-1 and/or HIV-2 viruses.

3. The immunodeficiency virus as claimed in one of claims 1 or 2, which retrovirus exhibits less reactivity with a monoclonal antibody directed against protein p 24, related to reverse transcriptase activity, than does the HIV-1 virus, and more activity, related to the activity of reverse transcriptase, than does HIV-2.

4. The immunodeficiency virus as claimed in one of the preceding claims, wherein antigen/antibody reactions with its transmembrane protein gp 41 are readily detectable using sera from patients originating from Africa, and wherein only a relatively small antigen/antibody reaction, or no such reaction, can be detected with the gp-41 using sera from patients originating from Germany.

5. The immunodeficiency virus as claimed in one of the abovementioned claims, which has an RNA sequence which is homologous to the extent of about 75% or more, based on the entire genome, with the RNA of the deposited virus.

6. The immunodeficiency virus as claimed in one of the abovementioned claims, which has an RNA sequence which is homologous to the extent of at least 75% with the RNA sequence of Table 1.

7. The immunodeficiency virus as claimed in one of claims 1 to 5, which has a nucleotide sequence which is homologous to the extent of at least 75% with the sequence of Table 3, or parts thereof.

8. The immunodeficiency virus as claimed in claim 7, wherein the part of the sequence is at least 50 nucleotides long.

9. The immunodeficiency virus as claimed in one of the preceding claims, which has a sequence or constituent sequence which corresponds to FIG. 4 or is homologous to this sequence, where the differences from the sequence given in FIG. 4, related to the gene loci, are at most: LTR: 17%, GAG: 29%, POL: 25%, VIF: 31%, ENV: 46%, NEF: 16%.

10. The immunodeficiency virus as claimed in one of the preceding claims, which has a sequence or constituent sequence which corresponds to FIG. 4 or is homologous to this sequence, where the differences from the sequence given in FIG. 4, related to the gene loci, are at most: LTR: 10%, GAG: 14%, POL: 12%, VIF: 15%, ENV: 22%, NEF: 10%.

11. cDNA which is complementary to the RNA, or parts thereof, of the immunodeficiency virus MVP-5180/91 deposited with the European Collection of Animal Cell Cultures (ECACC) under No. V 920 92 318, or of a virus as claimed in one of claims 1-10.

12. Recombinant DNA which contains cDNA as claimed in claim 11.

13. An antigen which was prepared using the cDNA as claimed in claim 11 or the recombinant DNA as claimed in claim 12, or using the amino acid structure which can be deduced from its cDNA.

14. The antigen as claimed in claim 13, which is a protein or peptide.

15. The antigen as claimed in one of claims 13 or 14, which has an amino acid sequence which corresponds to Table 3 or to a constituent sequence thereof.

16. The antigen as claimed in claim 15, wherein the constituent sequence has at least 10 amino acids.

17. The antigen as claimed in claim 15, which has the amino acid sequence RLQALETLIQNQQRLNLWGCKGKLICYTSVKWNTS, or a constituent sequence thereof having at least 6 consecutive amino acids.

18. An antigen which was prepared from an immunodeficiency virus as claimed in one of claims 1 to 10.

19. The antigen as claimed in one of claims 13 to 18, which was prepared recombinantly.

20. The antigen as claimed in one of claims 13 to 17, which was prepared synthetically.

21. A test kit for detecting antibodies against viruses which cause immuno deficiency, wherein antigen as claimed in claims 13 to 20 is employed.

22. The test kit as claimed in claim 21, which is a Western blot.

23. The test kit as claimed in claim 21, which is an ELISA test or a fluorescence-antibody detection test.

24. Use of the immunodeficiency virus as claimed in one of claims 1 to 10 and/or of the cDNA as claimed in claim 11 or 12 and/or of an antigen as claimed in claims 13 to 20 for detecting retroviruses which cause immune deficiency.

25. Use of a retrovirus as claimed in one of claims 1 to 10, of a cDNA as claimed in claim 11 or 12 and/or of an antigen as claimed in claims 13 to 20 for preparing vaccines.

26. Ribonucleic acid characterized in that the ribonucleic acid is coding for an immunodeficiency virus according to one of claims 1 to 10.

27. A process for detection of antibodies that specifically bind to at least one HIV retrovirus, said process comprising providing a sample containing at least one antibody obtained from a patient suspected of being infected with an HIV virus; providing at least one peptide comprising an amino acid sequence encoded by the genome of virus MvP-5180/91 (SEQ ID NO:56); combining said sample and said at least one peptide under conditions where said at least one peptide and said at least one antibody can specifically bind to each other; determining whether said at least one peptide and said at least one antibody specifically bound to each other; and optionally, quantifying the amount of binding between said at least one peptide and said at least one antibody.

28. The process of claim 27, wherein said process is an enzyme linked immunosorbent assay (ELISA).

29. The process of claim 27, wherein said sample is human serum.

30. The process of claim 27, wherein said process detects antibodies that specifically bind to an epitope of HIV-1.

31. The process of claim 27, wherein said process detects antibodies that specifically bind to an epitope of HIV-2.

32. The process of claim 27, wherein said process detects antibodies that specifically bind to an epitope of HIV-O.

33. The process of claim 27, wherein said process detects antibodies that specifically bind to an epitope of MvP-5180/91.

34. The process of claim 27, wherein said process detects antibodies that specifically bind to an epitope of a variant of MVP-5180/91.

35. The process of claim 27, wherein specific binding of said at least one antibody and said at least one peptide indicates the presence of an HIV virus in the body of the patient from whom said sample was taken.

36. The process of claim 35, wherein the process is a process for the diagnosis of HIV infection.

37. The process of claim 36, wherein said process diagnoses infection with HIV-1.

38. The process of claim 36, wherein said process diagnoses infection with HIV-2.

39. The process of claim 36, wherein said process diagnoses infection with HIV-O.

40. The process of claim 36, wherein said process diagnoses infection with HIV-1, HIV-2, and HIV-O.

41. The process of claim 27, wherein said process detects antibodies that specifically bind to an epitope of HIV-1, HIV-2, and HIV-3.

42. The process of claim 27, wherein said at least one peptide comprises a sequence present in SEQ ID NO:46.

43. The process of claim 27, wherein said at least one peptide comprises a sequence present in SEQ ID NO:39.

44. The process of claim 27, wherein said at least one peptide comprises a sequence present in SEQ ID NO:63.

45. The process of claim 27, wherein said at least one peptide comprises a sequence present in SEQ ID NO:62.

46. The process of claim 27, wherein said at least one peptide comprises a sequence present in SEQ ID NO:54.

47. The process of claim 27, wherein said at least one peptide comprises a sequence present in SEQ ID NO:55.

L5 ANSWER 3 OF 16 USPATFULL on STN
2003:3407 Retrovirus from the HIV group and its use.
Guertler, Lutz G., Muenchen, GERMANY, FEDERAL REPUBLIC OF
Eberle, Josef, Freising, GERMANY, FEDERAL REPUBLIC OF

Brunn, Albrecht V., Augsburg, GERMANY, FEDERAL REPUBLIC OF
Knapp, Stefan, Marburg-Wehrshausen, GERMANY, FEDERAL REPUBLIC OF
Hauser, Hans-Peter, Marburg, GERMANY, FEDERAL REPUBLIC OF
Dade Behring Marburg GmbH (U.S. corporation)
US 2003003442 A1 20030102
APPLICATION: US 2001-886149 A1 20010622 (9)
PRIORITY: DE 1992-4233646 19921006
DE 1992-4235718 19921022
DE 1992-4244541 19921230
DE 1993-4318186 19930601
DOCUMENT TYPE: Utility; APPLICATION.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A novel immunodeficiency virus is disclosed which has the designation MVP-5180/91 and which has been deposited with the European Collection of Animal Cell Cultures (ECACC) under No. V 920 52 318. The characteristic antigens which can be obtained from it and which can be employed for detecting antibodies against retroviruses which are associated with immunodeficiency diseases are also disclosed, as are the DNA and amino acid sequences of the virus.

CLM What is claimed is:

1) An immunodeficiency virus of the HIV group, or variants of this virus, which exhibits the essential morphological and immunological properties of the retrovirus which has the designation MVP-5180/91 and which has been deposited with the European Collection of Animal Cell Cultures (ECACC) under No. V 920 92 318.

2) The immunodeficiency virus as claimed in claim 1, which exhibits a protein band in a Western blot which corresponds to reverse transcriptase and is 3-7 kilodaltons smaller than the corresponding band of the HIV-1 and/or HIV-2 viruses.

3) The immunodeficiency virus as claimed in one of claim 1 or 2, which retrovirus exhibits less reactivity with a monoclonal antibody directed against protein p 24, related to reverse transcriptase activity, than does the HIV-1 virus, and more activity, related to the activity of reverse transcriptase, than does HIV-2.

4) The immunodeficiency virus as claimed in one of the preceding claims, wherein antigen/antibody reactions with its transmembrane protein gp 41 are readily detectable using sera from patients originating from Africa, and wherein only a relatively small antigen/antibody reaction, or no such reaction, can be detected with the gp-41 using sera from patients originating from Germany.

5) The immunodeficiency virus as claimed in one of the abovementioned claims, which has an RNA sequence which is homologous to the extent of about 75% or more, based on the entire genome, with the RNA of the deposited virus.

6) The immunodeficiency virus as claimed in one of the abovementioned claims, which has an RNA sequence which is homologous to the extent of at least 75% with the RNA sequence of Table 1.

7) The immunodeficiency virus as claimed in one of claims 1 to 5, which has a nucleotide sequence which is homologous to the extent of at least 75% with the sequence of Table 3, or parts thereof.

8) The immunodeficiency virus as claimed in claim 7, wherein the part of the sequence is at least 50 nucleotides long.

9) The immunodeficiency virus as claimed in one of the preceding claims, which has a sequence or constituent sequence which corresponds to FIG. 4 or is homologous to this sequence, where the differences from the sequence given in FIG. 4, related to the gene loci, are at most: LTR: 17%, GAG: 29%, POL: 25%, VIF: 31%, ENV: 46%, NEF: 16%.

10) The immunodeficiency virus as claimed in one of the preceding claims, which has a sequence or constituent sequence which corresponds to FIG. 4 or is homologous to this sequence, where the differences from the sequence given in FIG. 4, related to the gene loci, are at most: LTR: 10%, GAG: 14%, POL: 12%, VIF: 15%, ENV: 22%, NEF: 10%.

11) cDNA which is complementary to the RNA, or parts thereof, of the immunodeficiency virus MVP-5180/91 deposited with the European Collection of Animal Cell Cultures (ECACC) under No. V 920 92 318, or of a virus as claimed in one of claims 1-10.

12) Recombinant DNA which contains cDNA as claimed in claim 11.

13) An antigen which was prepared using the cDNA as claimed in claim 11 or the recombinant DNA as claimed in claim 12, or using the amino acid structure which can be deduced from its cDNA.

14) The antigen as claimed in claim 13, which is a protein or peptide.

15) The antigen as claimed in one of claim 13 or 14, which has an amino acid sequence which corresponds to Table 3 or to a constituent sequence thereof.

16) The antigen as claimed in claim 15, wherein the constituent sequence has at least 10 amino acids.

17) The antigen as claimed in claim 15, which has the amino acid sequence RLQALETLIQNQQRLNLWGCKGKLICYTSVKWNTS, or a constituent sequence thereof having at least 6 consecutive amino acids.

18) An antigen which was prepared from an immunodeficiency virus as claimed in one of claims 1 to 10.

19) The antigen as claimed in one of claims 13 to 18, which was prepared recombinantly.

20) The antigen as claimed in one of claims 13 to 17, which was prepared synthetically.

21) A test kit for detecting antibodies against viruses which cause immuno deficiency, wherein antigen as claimed in claims 13 to 20 is employed.

22) The test kit as claimed in claim 21, which is a Western blot.

23) The test kit as claimed in claim 21, which is an ELISA test or a fluorescence-antibody detection test.

24) Use of the immunodeficiency virus as claimed in one of claims 1 to 10 and/or of the cDNA as claimed in claim 11 or 12 and/or of an antigen as claimed in claims 13 to 20 for detecting retroviruses which cause immune deficiency.

25) Use of a retrovirus as claimed in one of claims 1 to 10, of a cDNA as claimed in claim 11 or 12 and/or of an antigen as claimed in claims 13 to 20 for preparing vaccines.

26) Ribonucleic acid characterized in that the ribonucleic acid is coding for an immunodeficiency virus according to one of claims 1 to 10.

27. Virus MvP-5180/91, deposited with the European Collection of Animal Cell Culture (ECACC) under No. V 920 92 318.

28. A variant virus, which is a variant of virus MvP-5180/91, wherein said variant has a genome that has a nucleotide sequence that shows at least 66% homology to SEQ ID NO:37 or SEQ ID NO:38.

29. The variant virus of claim 28, wherein said variant has a genome that has a nucleotide sequence that shows at least 75% homology to SEQ ID NO:37 or SEQ ID NO:38.

30. The variant virus of claim 28, wherein said variant has a genome that has a nucleotide sequence that shows at least 85% homology to SEQ ID NO:37 or SEQ ID NO:38.

31. A variant virus, which is a variant of virus MvP-5180/91, wherein said variant has a genome that has a nucleotide sequence that shows at least 66% homology to SEQ ID NO:44 or SEQ ID NO:45.

32. The variant virus of claim 31, wherein said variant has a genome that has a nucleotide sequence that shows at least 75% homology to SEQ ID NO:44 or SEQ ID NO:45.

33. The variant virus of claim 31, wherein said variant has a genome that has a nucleotide sequence that shows at least 85% homology to SEQ ID NO:44 or SEQ ID NO:45.

34. The variant virus of claim 31, wherein said variant has a genome that has a sequence that shows at least 66% homology to SEQ ID NO:44 or SEQ ID NO:45 over at least 50 nucleotides.

35. The variant virus of claim 34, wherein said variant has a genome that has a sequence that shows at least 66% homology to SEQ ID NO:44 or SEQ ID NO:45 over at least 100 nucleotides.

36. The variant virus of claim 31, wherein said variant has a genome that has a sequence that shows at least 75% homology to SEQ ID NO:44 or SEQ ID NO:45 over at least 50 nucleotides.

37. The variant virus of claim 36, wherein said variant has a genome that has a sequence that shows at least 75% homology to SEQ ID NO:44 or SEQ ID NO:45 over at least 100 nucleotides.

38. The variant virus of claim 31, wherein said variant has a genome that has a sequence that shows at least 85% homology to SEQ ID NO:44 or SEQ ID NO:45 over at least 50 nucleotides.

39. The variant virus of claim 38, wherein said variant has a genome that has a sequence that shows at least 85% homology to SEQ ID NO:44 or SEQ ID NO:45 over at least 100 nucleotides.

40. A variant virus, which is a variant of virus MvP-5180/91, wherein said variant has a genome that encodes a polypeptide that shows at least 66% homology to SEQ ID NO:39.

41. The variant virus of claim 40, wherein said variant has a genome that has a sequence that encodes a polypeptide that shows at least 75% homology to SEQ ID NO:39.

42. The variant virus of claim 40, wherein said variant has a genome that encodes a polypeptide that shows at least 85% homology to SEQ ID NQ:39.

43. A variant virus, which is a variant of virus MvP-5180/91, wherein said variant has a genome that encodes a polypeptide that shows at least 66% homology to SEQ ID NO:46.

44. The variant virus of claim 43, wherein said variant has a genome that encodes a polypeptide that shows at least 66% homology to SEQ ID NO:46 over at least 16 amino acid residues.

45. The variant virus of claim 44, wherein said variant has a genome

that encodes a polypeptide that shows at least 66% homology to SEQ ID NO:46 over at least 33 amino acid residues.

46. A variant virus, which is a variant of virus MvP-5180/91, wherein said variant has a genome that encodes a polypeptide that shows at least 75% homology to SEQ ID NO:46.

47. The variant virus of claim 46, wherein said variant has a genome that encodes a polypeptide that shows at least 75% homology to SEQ ID NO:46 over at least 16 amino acid residues.

48. The variant virus of claim 47, wherein said variant has a genome that encodes a polypeptide that shows at least 75% homology to SEQ ID NO:46 over at least 33 amino acid residues.

49. A variant virus, which is a variant of virus MvP-5180/91, wherein said variant has a genome that encodes a polypeptide that shows at least 85% homology to SEQ ID NO:46.

50. The variant virus of claim 49, wherein said variant has a genome that encodes a polypeptide that shows at least 85% homology to SEQ ID NO:46 over at least 16 amino acid residues.

51. The variant virus of claim 50, wherein said variant has a genome that encodes a polypeptide that shows at least 85% homology to SEQ ID NO:46 over at least 33 amino acid residues.

52. The virus of claim 28, wherein said virus has a reverse transcriptase that is magnesium dependent, but not manganese dependent.

53. A variant virus, which is a variant of virus MvP-5180/91, wherein said variant has a genome that has a nucleotide sequence that shows at least 98% homology to SEQ ID NO:57.

54. A variant virus, which is a variant of virus MvP-5180/91, wherein said variant has a genome that encodes a polypeptide that shows at least 97.8% homology to SEQ ID NO:59.

55. A variant virus, which is a variant of virus MvP-5180/91, wherein said variant has a genome that encodes a polypeptide that shows at least 77.8% homology to SEQ ID NO:54.

56. A variant virus, which is a variant of virus MvP-5180/91, wherein said variant has an LTR that shows at least 83% homology to the long terminal repeat (LTR) of virus MvP-5180/91.

57. The variant virus of claim 56, wherein said variant LTR shows at least 85% homology to the LTR of virus MvP-5180/91.

58. The variant virus of claim 56, wherein said variant LTR shows at least 90% homology to the LTR of virus MvP-5180/91.

59. A variant virus, which is a variant of virus MvP-5180/91, wherein said variant has a GAG gene that shows at least 71% homology to the GAG gene of virus MvP-5180/91.

60. The variant virus of claim 59, wherein said variant LTR shows at least 72% homology to the GAG gene of virus MvP-5180/91.

61. The variant virus of claim 59, wherein said variant LTR shows at least 86% homology to the LTR of virus MvP-5180/91.

62. A variant virus, which is a variant of virus MvP-5180/91, wherein said variant has a POL gene that shows at least 75% homology to the POL gene of virus MvP-5180/91.

63. The variant virus of claim 62, wherein said variant POL gene shows at least 86% homology to the POL gene of virus MvP-5180/91.

64. The variant virus of claim 62, wherein said variant POL gene shows at least 88% homology to the POL gene of virus MvP-5180/91.

65. A variant virus, which is a variant of virus MvP-5180/91, wherein said variant has a VIF gene that shows at least 68% homology to the VIF gene of virus MvP-5180/91.

66. The variant virus of claim 65, wherein said variant VIF gene shows at least 70% homology to the VIF gene of virus MvP-5180/91.

67. The variant virus of claim 65, wherein said variant VIF gene shows at least 85% homology to the VIF gene of virus MvP-5180/91.

68. A variant virus, which is a variant of virus MvP-5180/91, wherein said variant has an ENV gene that shows at least 54% homology to the ENV gene of virus MvP-5180/91.

69. The variant virus of claim 68, wherein said variant ENV gene shows at least 55% homology to the ENV gene of virus MvP-5180/91.

70. The variant virus of claim 68, wherein said variant ENV gene shows at least 88% homology to the ENV gene of virus MvP-5180/91.

71. A variant virus, which is a variant of virus MvP-5180/91, wherein said variant has an NEF gene that shows at least 55% homology to the NEF gene of virus MvP-5180/91.

72. The variant virus of claim 71, wherein said variant NEF gene shows at least 84% homology to the NEF gene of virus MvP-5180/91.

73. The variant virus of claim 71, wherein said variant NEF gene shows at least 88% homology to the NEF gene of virus MvP-5180/91.

74. The variant virus of claim 71, wherein said variant NEF gene shows at least 90% homology to the NEF gene of virus MvP-5180/91.

L5 ANSWER 4 OF 16 USPATFULL on STN
2002:307816 Retrovirus from the HIV group and its use.
Guertler, Lutz G., Muenchen, GERMANY, FEDERAL REPUBLIC OF
Eberle, Josef, Freising, GERMANY, FEDERAL REPUBLIC OF
Brunn, Albrecht V., Augsburg, GERMANY, FEDERAL REPUBLIC OF
Knapp, Stefan, Marburg-Wehrshausen, GERMANY, FEDERAL REPUBLIC OF
Hauser, Hans-Peter, Marburg, GERMANY, FEDERAL REPUBLIC OF
Dade Behring Marburg GmbH (non-U.S. corporation)
US 2002172939 A1 20021121
APPLICATION: US 2001-886150 A1 20010622 (9)
PRIORITY: DE 1992-4233646 19921006
DE 1992-4235718 19921022
DE 1992-4244541 19921230
DE 1993-4318186 19930601
DOCUMENT TYPE: Utility; APPLICATION.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A novel immunodeficiency virus is disclosed which has the designation MVP-5180/91 and which has been deposited with the European Collection of Animal Cell Cultures (ECACC) under No. V 920 52 318. The characteristic antigens which can be obtained from it and which can be employed for detecting antibodies against retroviruses which are associated with immunodeficiency diseases are also disclosed, as are the DNA and amino acid sequences of the virus.
CLM What is claimed is:
1. An immunodeficiency virus of the HIV group, or variants of this virus, which exhibits the essential morphological and immunological

properties of the retrovirus which has the designation MVP-5180/91 and which has been deposited with the European Collection of Animal Cell Cultures (ECACC) under No: V 920 92 318.

2) The immunodeficiency virus as claimed in claim 1, which exhibits a protein band in a Western blot which corresponds to reverse transcriptase and is 3-7 kilodaltons smaller than the corresponding band of the HIV-1 and/or HIV-2 viruses.

3) The immunodeficiency virus as claimed in one of claims 1 or 2, which retrovirus exhibits less reactivity with a monoclonal antibody directed against protein p 24, related to reverse transcriptase activity, than does the HIV-1 virus, and more activity, related to the activity of reverse transcriptase, than does HIV-2.

4) The immunodeficiency virus as claimed in one of the preceding claims, wherein antigen/antibody reactions with its transmembrane protein gp 41 are readily detectable using sera from patients originating from Africa, and wherein only a relatively small antigen/antibody reaction, or no such reaction, can be detected with the gp-41 using sera from patients originating from Germany.

5) The immunodeficiency virus as claimed in one of the abovementioned claims, which has an RNA sequence which is homologous to the extent of about 75% or more, based on the entire genome, with the RNA of the deposited virus.

6) The immunodeficiency virus as claimed in one of the abovementioned claims, which has an RNA sequence which is homologous to the extent of at least 75% with the RNA sequence of Table 1.

7) The immunodeficiency virus as claimed in one of claims 1 to 5, which has a nucleotide sequence which is homologous to the extent of at least 75% with the sequence of Table 3, or parts thereof.

8) The immunodeficiency virus as claimed in claim 7, wherein the part of the sequence is at least 50 nucleotides long.

9) The immunodeficiency virus as claimed in one of the preceding claims, which has a sequence or constituent sequence which corresponds to FIG. 4 or is homologous to this sequence, where the differences from the sequence given in FIG. 4, related to the gene loci, are at most: LTR: 17%, GAG: 29%, POL: 25%, VIF: 31%, ENV: 46%, NEF: 16%.

10) The immunodeficiency virus as claimed in one of the preceding claims, which has a sequence or constituent sequence which corresponds to FIG. 4 or is homologous to this sequence, where the differences from the sequence given in FIG. 4, related to the gene loci, are at most: LTR: 10%, GAG: 14%, POL: 12%, VIF: 15%, ENV: 22%, NEF: 10%.

11) cDNA which is complementary to the RNA, or parts thereof, of the immunodeficiency virus MVP-5180/91 deposited with the European Collection of Animal Cell Cultures (ECACC) under No. V 920 92 318, or of a virus as claimed in one of claims 1-10.

12) Recombinant DNA which contains cDNA as claimed in claim 11.

13) An antigen which was prepared using the CDNA as claimed in claim 11 or the recombinant DNA as claimed in claim 12, or using the amino acid structure which can be deduced from its cDNA.

14) The antigen as claimed in claim 13, which is a protein or peptide.

15) The antigen as claimed in one of claims 13 or 14, which has an amino acid sequence which corresponds to Table 3 or to a constituent sequence thereof.

16) The antigen as claimed in claim 15, wherein the constituent sequence has at least 10 amino acids.

17) The antigen as claimed in claim 15, which has the amino acid sequence RLQALETLIQNQQRLNLWGCKGKLICYTSVKWNTS, or a constituent sequence thereof having at least 6 consecutive amino acids.

18) An antigen which was prepared from an immunodeficiency virus as claimed in one of claims 1 to 10.

19) The antigen as claimed in one of claims 13 to 18, which was prepared recombinantly.

20) The antigen as claimed in one of claims 13 to 17, which was prepared synthetically.

21) A test kit for detecting antibodies against viruses which cause immuno deficiency, wherein antigen as claimed in claims 13 to 20 is employed.

22) The test kit as claimed in claim 21, which is a Western blot.

23) The test kit as claimed in claim 21, which is an ELISA test or a fluorescence-antibody detection test.

24) Use of the immunodeficiency virus as claimed in one of claims 1 to 10 and/or of the CDNA as claimed in claim 11 or 12 and/or of an antigen as claimed in claims 13 to 20 for detecting retroviruses which cause immune deficiency.

25) Use of a retrovirus as claimed in one of claims 1 to 10, of a cDNA as claimed in claim 11 or 12 and/or of an antigen as claimed in claims 13 to 20 for preparing vaccines.

26) Ribonucleic acid characterized in that the ribonucleic acid is coding for an immunodeficiency virus according to one of claims 1 to 10.

27. A nucleic acid comprising the sequence of the genome of virus MvP-5180/91 (SEQ ID NO:56).

28. The nucleic acid of claim 27, wherein said nucleic acid is DNA.

29. The nucleic acid of claim 27, wherein said nucleic acid is RNA.

30. A nucleic acid comprising the sequence of SEQ ID NO:38 or SEQ ID NO:39.

31. A nucleic acid comprising the sequence of SEQ ID NO:44 or SEQ ID NO:45.

32. A nucleic acid comprising a nucleotide sequence having more than 66% homology with SEQ ID NO:44 or SEQ ID NO:45, over the length of SEQ ID NO:44 or SEQ ID NO:45, respectively.

33. The nucleic acid of claim 32, wherein said nucleic acid comprises a nucleotide sequence having more than 75% homology with SEQ ID NO:44 or SEQ ID NO:45, over the length of SEQ ID NO:44 or SEQ ID NO:45, respectively.

34. The nucleic acid of claim 33, wherein said nucleic acid comprises a nucleotide sequence having more than 85% homology with SEQ ID NO:44 or SEQ ID NO:45, over the length of SEQ ID NO:44 or SEQ ID NO:45, respectively.

35. A nucleic acid comprising a nucleotide sequence having more than 66%

homology with SEQ ID NO:37 or SEQ ID NO:38, over the length of SEQ ID NO:37 or SEQ ID NO:38, respectively.

36. The nucleic acid of claim 35, wherein said nucleic acid comprises a nucleotide sequence having more than 75% homology with SEQ ID NO:37 or SEQ ID NO:38, over the length of SEQ ID NO:37 or SEQ ID NO:38, respectively.

37. The nucleic acid of claim 36, wherein said nucleic acid comprises a nucleotide sequence having more than 85% homology with SEQ ID NO:37 or SEQ ID NO:38, over the length of SEQ ID NO:37 or SEQ ID NO:38, respectively.

38. A nucleic acid comprising at least 50 consecutive nucleotides of SEQ ID NO:56.

39. The nucleic acid of claim 38, said nucleic acid comprising at least 100 consecutive nucleotides of SEQ ID NO:56.

L5 ANSWER 5 OF 16 USPATFULL on STN
2002:279994 Retrovirus from the HIV group and its use.
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Eberle, Josef, Freising, GERMANY, FEDERAL REPUBLIC OF
Brunn, Albrecht V., Augsburg, GERMANY, FEDERAL REPUBLIC OF
Knapp, Stefan, Marburg-Wehrshausen, GERMANY, FEDERAL REPUBLIC OF
Hauser, Hans-Peter, Marburg, GERMANY, FEDERAL REPUBLIC OF
Dade Behring Marburg GmbH. (non-U.S. corporation)
US 2002155428 A1 20021024
APPLICATION: US 2001-886156 A1 20010622 (9)
PRIORITY: DE 1992-4233646 19921006
DE 1992-4235718 19921022
DE 1992-4244541 19921230
DE 1993-4318186 19930601
DOCUMENT TYPE: Utility; APPLICATION.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A novel immunodeficiency virus is disclosed which has the designation MVP-5180/91 and which has been deposited with the European Collection of Animal Cell Cultures (ECACC) under No. V 920 52 318. The characteristics antigens which can be obtained from it and which can be employed for detecting antibodies against retroviruses which are associated with immunodeficiency diseases are also disclosed, as are the DNA and amino acid sequences of the virus.
CLM What is claimed is:
1) an immunodeficiency virus of the HIV group, or variants of this virus, which exhibits the essential morphological and immunological properties of the retrovirus which has the designation MVP-5180/91 and which has been deposited with the European collection of animal cell cultures (ECACC) under no: V 920 92 318.

2) The immunodeficiency virus as claimed in claim 1, which exhibits a protein band in a Western blot which corresponds to reverse transcriptase and is 3-7 kilodaltons smaller than the corresponding band of the HIV-1 and/or HIV-2 viruses.

3) The immunodeficiency virus as claimed in one of claim 1 or 2, which retrovirus exhibits less reactivity with a monoclonal antibody directed against protein p 24, related to reverse transcriptase activity, than does the HIV-1 virus, and more activity, related to the activity of reverse transcriptase, than does HIV-2.

4) The immunodeficiency virus as claimed in one of the preceding claims, wherein antigen/antibody reactions with its transmembrane protein gp 41 are readily detectable using sera from patients originating from Africa, and wherein only a relatively small antigen/antibody reaction, or no such reaction, can be detected with the gp-41 using sera from patients

originating from Germany.

5) The immunodeficiency virus as claimed in one of the abovementioned claims, which has an RNA sequence which is homologous to the extent of about 75% or more, based on the entire genome, with the RNA of the deposited virus.

6) The immunodeficiency virus as claimed in one of the abovementioned claims, which has an RNA sequence which is homologous to the extent of at least 75% with the RNA sequence of Table 1.

7) The immunodeficiency virus as claimed in one of claims 1 to 5, which has a nucleotide sequence which is homologous to the extent of at least 75% with the sequence of Table 3, or parts thereof.

8) The immunodeficiency virus as claimed in claim 7, wherein the part of the sequence is at least 50 nucleotides long.

9) The immunodeficiency virus as claimed in one of the preceding claims, which has a sequence or constituent sequence which corresponds to FIG. 4 or is homologous to this sequence, where the differences from the sequence given in FIG. 4, related to the gene loci, are at most: LTR: 17%, GAG: 29%, POL: 25%, VIF: 31%, ENV: 46%, NEF: 16%.

10) The immunodeficiency virus as claimed in one of the preceding claims, which has a sequence or constituent sequence which corresponds to FIG. 4 or is homologous to this sequence, where the differences from the sequence given in FIG. 4, related to the gene loci, are at most: LTR: 10%, GAG: 14%, POL: 12%, VIF: 15%, ENV: 22%, NEF: 10%.

11) cDNA which is complementary to the RNA, or parts thereof, of the immunodeficiency virus MVP-5180/91 deposited with the European Collection of Animal Cell Cultures (ECACC) under No. V 920 92 318, or of a virus as claimed in one of claims 1-10.

12) Recombinant DNA which contains cDNA as claimed in claim 11.

13) An antigen which was prepared using the cDNA as claimed in claim 11 or the recombinant DNA as claimed in claim 12, or using the amino acid structure which can be deduced from its cDNA.

14) The antigen as claimed in claim 13, which is a protein or peptide.

15) The antigen as claimed in one of claim 13 or 14, which has an amino acid sequence which corresponds to Table 3 or to a constituent sequence thereof.

16) The antigen as claimed in claim 15, wherein the constituent sequence has at least 10 amino acids.

17) The antigen as claimed in claim 15, which has the amino acid sequence RLQALETLIQNQQRLNLWGCKGKLICYTSVKWNTS, or a constituent sequence thereof having at least 6 consecutive amino acids.

18) An antigen which was prepared from an immunodeficiency virus as claimed in one of claims 1 to 10.

19) The antigen as claimed in one of claims 13 to 18, which was prepared recombinantly.

20) The antigen as claimed in one of claims 13 to 17, which was prepared synthetically.

21) A test kit for detecting antibodies against viruses which cause immuno deficiency, wherein antigen as claimed in claims 13 to 20 is employed.

22) The test kit as claimed in claim 21, which is a Western blot.

23) The test kit as claimed in claim 21, which is an ELISA test or a fluorescence-antibody detection test.

24) Use of the immunodeficiency virus as claimed in one of claims 1 to 10 and/or of the cDNA as claimed in claim 11 or 12 and/or of an antigen as claimed in claims 13 to 20 for detecting retroviruses which cause immune deficiency.

25) Use of a retrovirus as claimed in one of claims 1 to 10, of a cDNA as claimed in claim 11 or 12 and/or of an antigen as claimed in claims 13 to 20 for preparing vaccines.

26) Ribonucleic acid characterized in that the ribonucleic acid is coding for an immunodeficiency virus according to one of claims 1 to 10.

27. A peptide antigen comprising an amino acid sequence encoded by SEQ ID NO:56.

28. The antigen of claim 27, wherein said amino acid sequence is at least 6 residues in length.

29. The antigen of claim 27, wherein said amino acid sequence is at least 10 residues in length.

30. The antigen of claim 27, wherein said amino acid sequence is at least 15 residues in length.

31. The antigen of claim 27, wherein said amino acid sequence is at least 16 residues in length.

32. The antigen of claim 27, wherein said amino acid sequence is at least 33 residues in length.

33. The antigen of claim 27, wherein said antigen comprises an amino acid sequence that is encoded by nucleotides 817-2310 of SEQ ID NO:56.

34. The antigen of claim 27, wherein said antigen comprises an amino acid sequence that is encoded by nucleotides 2073-5153 of SEQ ID NO:56.

35. The antigen of claim 27, wherein said antigen comprises an amino acid sequence that is encoded by nucleotides 6260-8887 of SEQ ID NO:56.

36. A peptide antigen comprising the amino acid sequence of SEQ ID NO:46.

37. A peptide antigen comprising an amino acid sequence present in SEQ ID NO:46.

38. The antigen of claim 37, wherein said amino acid sequence is at least 6 residues in length.

39. The antigen of claim 37, wherein said amino acid sequence is at least 10 residues in length.

40. The antigen of claim 37, wherein said amino acid sequence is at least 15 residues in length.

41. The antigen of claim 37, wherein said amino acid sequence is at least 16 residues in length.

42. The antigen of claim 37, wherein said amino acid sequence is at least 33 residues in length.

43. A peptide antigen comprising the amino acid sequence of SEQ ID NO:39.

44. A peptide antigen comprising an amino acid sequence present in SEQ ID NO:39.

45. The antigen of claim 44, wherein said amino acid sequence is at least 6 residues in length.

46. The antigen of claim 44, wherein said amino acid sequence is at least 10 residues in length.

47. The antigen of claim 44, wherein said amino acid sequence is at least 15 residues in length.

48. The antigen of claim 44, wherein said amino acid sequence is at least 16 residues in length.

49. The antigen of claim 44, wherein said amino acid sequence is at least 33 residues in length.

50. A peptide antigen comprising the amino acid sequence of SEQ ID NO:63.

51. A peptide antigen comprising an amino acid sequence present in SEQ ID NO:63.

52. The antigen of claim 51, wherein said amino acid sequence is at least 6 residues in length.

53. The antigen of claim 51, wherein said amino acid sequence is at least 10 residues in length.

54. The antigen of claim 51, wherein said amino acid sequence is at least 15 residues in length.

55. The antigen of claim 51, wherein said amino acid sequence is at least 16 residues in length.

56. A peptide antigen comprising the sequence of SEQ ID NO:62.

57. A peptide antigen comprising an amino acid sequence present in SEQ ID NO:62.

58. The antigen of claim 57, wherein said amino acid sequence is at least 6 residues in length.

59. The antigen of claim 57, wherein said amino acid sequence is at least 10 residues in length.

60. The antigen of claim 57, wherein said amino acid sequence is at least 15 residues in length.

61. The antigen of claim 57, wherein said amino acid sequence is at least 16 residues in length.

62. The antigen of claim 57, wherein said amino acid sequence is at least 33 residues in length.

63. A peptide antigen comprising the sequence of SEQ ID NO:59.

64. A peptide antigen comprising an amino acid sequence present in SEQ ID NO:59.

65. The antigen of claim 64, wherein said amino acid sequence is at least 6 residues in length.

66. The antigen of claim 64, wherein said amino acid sequence is at least 10 residues in length.

67. The antigen of claim 64, wherein said amino acid sequence is at least 15 residues in length.

68. The antigen of claim 64, wherein said amino acid sequence is at least 16 residues in length.

69. The antigen of claim 64, wherein said amino acid sequence is at least 33 residues in length.

70. A peptide antigen comprising the sequence of SEQ ID NO:60.

71. A peptide antigen comprising an amino acid sequence present in SEQ ID NO:60.

72. The antigen of claim 71, wherein said amino acid sequence is at least 6 residues in length.

73. The antigen of claim 71, wherein said amino acid sequence is at least 10 residues in length.

74. The antigen of claim 71, wherein said amino acid sequence is at least 15 residues in length.

75. The antigen of claim 71, wherein said amino acid sequence is at least 16 residues in length.

76. The antigen of claim 71, wherein said amino acid sequence is at least 33 residues in length.

77. A peptide antigen comprising the amino acid sequence of SEQ ID NO:54.

78. A peptide antigen comprising an amino acid sequence present in SEQ ID NO:54.

79. The antigen of claim 78, wherein said amino acid sequence is at least 6 residues in length.

80. The antigen of claim 78, wherein said amino acid sequence is at least 10 residues in length.

81. The antigen of claim 78, wherein said amino acid sequence is at least 15 residues in length.

82. The antigen of claim 78, wherein said amino acid sequence is at least 16 residues in length.

83. The antigen of claim 78, wherein said amino acid sequence is at least 33 residues in length.

84. A peptide antigen comprising the amino acid sequence of SEQ ID NO:55.

85. A peptide antigen comprising an amino acid sequence present in SEQ ID NO:55.

86. The antigen of claim 85, wherein said amino acid sequence is at least 6 residues in length.

87. The antigen of claim 85, wherein said amino acid sequence is at least 10 residues in length.

88. The antigen of claim 85, wherein said amino acid sequence is at least 15 residues in length.

89. The antigen of claim 85, wherein said amino acid sequence is at least 16 residues in length.

90. The antigen of claim 85, wherein said amino acid sequence is at least 33 residues in length.

91. A peptide antigen comprising a peptide present in the GAG protein of MvP-5180/91.

92. A peptide antigen comprising a peptide present in the POL protein of MvP-5180/91.

93. A peptide antigen comprising a peptide present in the VIF protein of MvP-5180/91.

94. A peptide antigen comprising a peptide present in the ENV protein of MvP-5180/91.

95. A peptide antigen comprising a peptide present in the NEF protein of MvP-5180/91.

L5 ANSWER 6 OF 16 USPATFULL on STN
2002:174793 Toxoplasma gondii antigens, the preparation thereof and the use thereof.
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Ziegelmaier, Robert, Marburg, GERMANY, FEDERAL REPUBLIC OF
Kupper, Hans, Marburg, GERMANY, FEDERAL REPUBLIC OF
Dade Behring Marburg GmbH, Marburg, GERMANY, FEDERAL REPUBLIC OF (non-U.S. corporation)
US 6419925 B1 20020716
APPLICATION: US 2001-968927 20011003 (9)
PRIORITY: DE 1989-3940598 19891208
DOCUMENT TYPE: Utility; GRANTED.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to the identification of toxoplasma gondii antigens and the preparation thereof by genetic engineering. A cDNA expression gene bank of this parasite was prepared. Recombinant clones which are of diagnostic interest were identified using a high-titer rabbit anti-Toxoplasma gondii serum, and isolated.
CLM What is claimed is:
1. A diagnostic which contains a monoclonal antibody or polyclonal antibody which specifically binds a substantially purified protein comprising at least one amino acid sequence selected from SEQ ID NOS: 2, 4, 6, 8, 10, 12, 16, 18, or 20, and immunogenic fragments thereof.

2. The diagnostic of claim 1, wherein the monoclonal antibody or polyclonal antibody specifically binds a substantially purified protein comprising SEQ ID NO:2.

3. The diagnostic of claim 1, wherein the monoclonal antibody or polyclonal antibody specifically binds a substantially purified protein comprising SEQ ID NO:4.

4. The diagnostic of claim 1, wherein the monoclonal antibody or polyclonal antibody specifically binds a substantially purified protein comprising SEQ ID NO:6.

5. The diagnostic of claim 1, wherein the monoclonal antibody or polyclonal antibody specifically binds a substantially purified protein comprising SEQ ID NO:8.

6. The diagnostic of claim 1, wherein the monoclonal antibody or

polyclonal antibody specifically binds a substantially purified protein comprising SEQ ID NO:10.

7. The diagnostic of claim 1, wherein the monoclonal antibody or polyclonal antibody specifically binds a substantially purified protein comprising SEQ ID NO:12.

8. The diagnostic of claim 1, wherein the monoclonal antibody or polyclonal antibody specifically binds a substantially purified protein comprising SEQ ID NO:16.

9. The diagnostic of claim 1, wherein the monoclonal antibody or polyclonal antibody specifically binds a substantially purified protein comprising SEQ ID NO:18.

10. The diagnostic of claim 1, wherein the monoclonal antibody or polyclonal antibody specifically binds a substantially purified protein comprising SEQ ID NO:20.

11. A diagnostic which contains a monoclonal antibody or polyclonal antibody which specifically binds a substantially purified protein comprising an amino acid sequence encoded by a DNA sequence of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 14, 15, 17, or 19.

12. The diagnostic of claim 11, wherein the monoclonal antibody or polyclonal antibody specifically binds a substantially purified protein comprising an amino acid sequence encoded by a DNA sequence of SEQ ID NO: 1.

13. The diagnostic of claim 11, wherein the monoclonal antibody or polyclonal antibody specifically binds a substantially purified protein comprising an amino acid sequence encoded by a DNA sequence of SEQ ID NO: 3.

14. The diagnostic of claim 11, wherein the monoclonal antibody or polyclonal antibody specifically binds a substantially purified protein comprising an amino acid sequence encoded by a DNA sequence of SEQ ID NO: 5.

15. The diagnostic of claim 11, wherein the monoclonal antibody or polyclonal antibody specifically binds a substantially purified protein comprising an amino acid sequence encoded by a DNA sequence of SEQ ID NO: 7.

16. The diagnostic of claim 11, wherein the monoclonal antibody or polyclonal antibody specifically binds a substantially purified protein comprising an amino acid sequence encoded by a DNA sequence of SEQ ID NO: 9.

17. The diagnostic of claim 11, wherein the monoclonal antibody or polyclonal antibody specifically binds a substantially purified protein comprising an amino acid sequence encoded by a DNA sequence of SEQ ID NO: 11.

18. The diagnostic of claim 11, wherein the monoclonal antibody or polyclonal antibody specifically binds a substantially purified protein comprising an amino acid sequence encoded by a DNA sequence of SEQ ID NO: 13.

19. The diagnostic of claim 11, wherein the monoclonal antibody or polyclonal antibody specifically binds a substantially purified protein comprising an amino acid sequence encoded by a DNA sequence of SEQ ID NO: 14.

20. The diagnostic of claim 11, wherein the monoclonal antibody or polyclonal antibody specifically binds a substantially purified protein

comprising an amino acid sequence encoded by a DNA sequence of SEQ ID NO: 15.

21. The diagnostic of claim 11, wherein the monoclonal antibody or polyclonal antibody specifically binds a substantially purified protein comprising an amino acid sequence encoded by a DNA sequence of SEQ ID NO: 17.

22. The diagnostic of claim 11, wherein the monoclonal antibody or polyclonal antibody specifically binds a substantially purified protein comprising an amino acid sequence encoded by a DNA sequence of SEQ ID NO: 19.

ANSWER 7 OF 16 USPATFULL on STN

01:220699 Toxoplasma gondii antigens, the preparation thereof and the use thereof.

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Ziegelmaier, Robert, Marburg, Germany, Federal Republic of
Kupper, Hans, Marburg, Germany, Federal Republic of
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US 6326008 B1 20011204
APPLICATION: US 1999-461240 19991216 (9)
PRIORITY: DE 1989-3940598 19891208
DOCUMENT TYPE: Utility; GRANTED.
S INDEXING IS AVAILABLE FOR THIS PATENT.

The present invention relates to the identification of toxoplasma gondii antigens and the preparation thereof by genetic engineering. A cDNA expression gene bank of this parasite was prepared. Recombinant clones which are of diagnostic interest were identified using a high-titer rabbit anti-Toxoplasma gondii serum, and isolated.

M What is claimed is:

1. A diagnostic for detecting a toxoplasmosis infection, which contains a substantially purified protein comprising (a) at least one amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 16, 18, or 20, and immunogenic fragments thereof, or (b) an amino acid sequence encoded by a DNA sequence of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 14, 15, 17, or 19.

2. A diagnostic which comprises at least one nucleic acid sequence consisting of a SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 14, 15, 17, or 19 or at least one isolated nucleic acid molecule which encodes a protein comprising the amino acid sequence of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 16, 18, or 20.

3. A diagnostic as claimed in claim 1, wherein the at least one amino acid sequence is selected from the group consisting of SEQ ID NOS: 4 and 12 and immunogenic fragments thereof, or wherein the amino acid sequence encoded by a DNA sequence is selected from the group consisting of SEQ ID NOS: 3 and 11.

4. A process for detecting a toxoplasmosis infection, comprising contacting a body fluid with a diagnostic as claimed in claim 1, and detecting binding of antibodies in the body fluid to the diagnostic, wherein the presence of antibodies indicates the presence of a toxoplasmosis infection.

5. A process for detecting a toxoplasmosis infection, comprising contacting a body fluid with a diagnostic as claimed in claim 3, and detecting binding of antibodies in the body fluid to the diagnostic, wherein the presence of antibodies indicates the presence of a toxoplasmosis infection.

ANSWER 8 OF 16 USPATFULL on STN

2001:136366 Diagnostic assay for detection of HIV.
Guertler, Lutz G., Munich, Germany, Federal Republic of
Eberle, Josef, Freising, Germany, Federal Republic of
Brunn, Albrecht v., Augsburg, Germany, Federal Republic of
Knapp, Stefan, Marburg-Wehrshausen, Germany, Federal Republic of
Hauser, Hans-Peter, Marburg, Germany, Federal Republic of
Dade Behring Marburg GmbH, Marburg, Germany, Federal Republic of (non-U.S. corporation)
US 6277561 B1 20010821
APPLICATION: US 1998-109916 19980702 (9)
PRIORITY: DE 1992-4233646 19921006
DE 1992-4235718 19921022
DE 1992-4244541 19921230
DE 1993-4318186 19930601
DOCUMENT TYPE: Utility; GRANTED.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB A novel immunodeficiency virus is disclosed which has the designation MVP-5180/91 and which has been deposited with the European Collection of Animal Cell Cultures (ECACC) under No. V 920 92 318. The characteristic antigens which can be obtained from it and which can be employed for detecting antibodies against retroviruses which are associated with immuno-deficiency diseases are also disclosed, as are the DNA and amino acid sequences of the virus.

CLM What is claimed is:

1. A method of detecting the presence of at least one retrovirus in a sample, said method comprising: (a) combining a sample with an oligonudeotide whose sequence is present within the sequence of SEQ ID NO:56 or the complement of SEQ ID NO:56; and (b) detecting hybridization of said oligonucleotide to nucleic acid present in said sample, wherein hybridization of said oligonucleotide to nucleic acid present in said sample indicates the presence of at least one retrovirus in said sample.

2. The method of claim 1, wherein said detecting includes amplification of retroviral nucleic acid.

3. The method of claim 2, wherein said amplification is acellular amplification.

4. The method of claim 3, wherein said acellular amplification includes the Polymerase Chain Reaction.

5. The method of claim 1, wherein said sample comprises biological material from a human.

6. The method of claim 1, wherein said oligonucleotide specifically binds to nucleic acid of at least one HIV retrovirus group.

7. The method of claim 6, wherein the method detects more than one HIV group.

8. The method of claim 6, wherein said at least one HIV retrovirus is selected from the group consisting of HIV-1, HIV-2, and HIV-0.

9. The method of claim 8, wherein said method detects at least HIV-1 and HIV-0.

10. The method of claim 8, wherein said method detects at least HIV-2 and HIV-0.

11. The method of claim 8, wherein said method detects HIV-1, HIV-2, and HIV-0.

12. The method of claim 1, wherein said oligonucleotide is selected from the group consisting of SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID

NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:64, and SEQ ID NO:65.

13. The method of claim 1, wherein said oligonucleotide encodes at least 6 contiguous amino adds of SEQ ID NO:39, SEQ ID NO:46, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:59, SEQ iD NO:60, SEQ ID NO:62, or SEQ ID NO:63.

14. The method of claim 1, wherein said oligonucleotide sequence is present within the sequence of SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:57, or SEQ ID NO:58, or the complementary sequences thereof.

15. The method of claim 1, wherein said oligonucleotide is from approximately 17 to 42 bases in length.

16. The method of claim 1, wherein said oligonucleotide is from approximately 20 to 25 bases in length.

17. The method of claim 1, wherein said oligonudeotide is selected from within nucleotides 817-2310 of SEQ ID NO:56, nucleofides 2073-5153 of SEQ ID NO:56, or nucleotides 6260-8887 of SEQ ID NO:56.

18. An oligonucleotide having a sequence present within the sequence of SEQ ID NO:56 or the complement of SEQ ID NO:56, wherein said oligonucleotide is at least 17 nucleotides in length.

19. The oligonucleotide of claim 18, selected from the group consisting of SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:1 8, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:64, and SEQ ID NO:65.

20. The oligonucleotide of claim 18, wherein said oligonucleotide sequence is present within the sequence of SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:57, or SEQ ID NO:58, or the complementary sequences thereof.

21. The oligonucleotide of claim 18, wherein said oligonucleotide can encode at least 6 contiguous amino acids of SEQ ID NO:39, SEQ ID NO:46, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:62, or SEQ ID NO:63.

22. The oligonucleotide of claim 18, wherein said oligonucleotide is from approximately 17 to 42 bases in length.

23. The oligonucleotide of claim 22, wherein said oligonucleotide is from approximately 20 to 25 bases in length.

24. A method of detecting the presence of an immunodeficiency virus of the HIV group, or variants of said virus, which exhibits all the essential morphological and immunological properties of the retrovirus which has the designation MVP-5180/91 and which has been deposited with the European Collection of Animal Cell Cultures (ECAC) under No. V 920 92 318, wherein said method comprises: (a) combining a sample with an oligonucleotide whose sequence is present within the sequence of SEQ ID NO:56 or the complement of SEQ ID NO:56; and (b) detecting hybridization of said oligonucleotide to nucleic acid present in said sample, wherein hybridization of said oligonucleotide to nucleic acid present in said sample indicates the presence of said immunodeficiency virus MVP-5 180/91, or variants of said virus.

25. The method of claim 24, wherein said detecting includes amplification of said nucleic acid present in said sample.

26. The method of claim 24, further comprising detecting at least one virus selected from the group consisting of HIV-1 and HIV-2.

27. The method of claim 24 wherein said oligonucleotide sequence can encode at least 6 contiguous amino acids of SEQ ID NO:39, SEQ ID NO:46, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:62, or SEQ ID NO:63.

28. The method of claim 24, wherein said oligonucleotide is selected from within nucleotides 817-2310 of SEQ ID NO:56, nucleotides 2073-5153 of SEQ ID NO:56, or nucleotides 6260-8887 of SEQ ID NO:56.

29. A method of detecting the presence of at least one retrovirus in a sample, said method comprising: (a) combining a sample with an oligonucleotide whose sequence is present within the sequence of SEQ ID NO:56 or the complement of SEQ ID NO:56, or a variant thereof; and (b) detecting hybridization of said oligonucleotide to nucleic acid present in said sample, wherein said variant shows more than 66% homology to at least one region of SEQ ID NO:56 which is at least 50 nucleotides in length, and wherein hybridization of said oligonucleotide to nucleic acid present in said sample indicates the presence of at least one retrovirus in said sample.

30. The method of claim 29, wherein the region of SEQ ID NO:56 to which the variant shows homology is between 50 and 100 nucleotides in length.

31. The method of claim 29, wherein said variant shows more than 75% homology to at least one region of SEQ ID NO:56.

32. The method of claim 29, wherein said variant shows more than 85% homology to at least one region of SEQ ID NO:56.

33. The method of claim 29, wherein said oligonucleotide is from approximately 17 to 42 bases in length.

34. The method of claim 29, wherein said oligonucleotide is from approximately 20 to 25 bases in length.

35. The method of claim 29, wherein said oligonucleotide encodes at least 6 contiguous amino acids of SEQ ID NO:39, SEQ ID NO:46, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:62, or SEQ ID NO:63.

36. The method of claim 29, wherein said oligonucleotide is selected from within nucleotides 817-2310 of SEQ ID NO:56, nucleotides 2073-5153 of SEQ ID NO:56, or nucleotides 6260-8887 of SEQ ID NO:56.

37. The method of claim 29, wherein said detecting includes amplification of retroviral nucleic acid.

38. The method of claim 37, wherein said amplification is a cellular amplification.

39. The method of claim 38, wherein said acellular amplification includes the Polymerase Chain Reaction.

40. The method of claim 29, wherein said sample comprises biological material from a human.

41. The method of claim 29, wherein said oligonucleotide specifically binds to nucleic acid of at least one HIV retrovirus group.

42. The method of claim 41, wherein the method detects more than one HIV group.

43. The method of claim 41, wherein said at least one HIV retrovirus is selected from the group consisting of HIV-1, HIV-2, and HIV-0.

44. The method of claim 43, wherein said method detects at least HIV-1 and HIV-0.

45. The method of claim 43, wherein said method detects at least HIV-2 and HIV-0.

46. The method of claim 43, wherein said method detects HIV-1, HIV-2, and HIV-0.

47. The method of claim 29, wherein said oligonucleotide encodes at least 6 contiguous amino acids of the GAG protein encoded by nucleotides 817-2310 of SEQ ID NO:56.

48. The method of claim 29, wherein said oligonucleotide encodes at least 6 contiguous amino acids of the POL protein encoded by nucleotides 2073-5153 of SEQ ID NO:56.

49. The method of claim 29, wherein said oligonucleotide encodes at least 6 contiguous amino acids of the ENV protein encoded by nucleotides 6260-8887 of SEQ ID NO:56.

50. The method of claim 29, wherein said at least one retrovirus is HIV-0.

51. A method of detecting the presence of an immunodeficiency virus of the HIV group which has the designation MVP-5180/91 and which has been deposited with the European Collection of Animal Cell Cultures (ECAC) under No. V 920 92 318, or variants of said virus, wherein said variants have nucleic acid which shows more than 66% homology to SEQ ID NO:56, wherein said method comprises: (a) combining a sample with an oligonucleotide whose sequence is present within the sequence of SEQ ID NO:56 or the complement of SEQ ID NO:56; and (b) detecting hybridization of said oligonucleotide to nucleic acid present in said sample, wherein hybridization of said oligonucleotide to nucleic acid present in said sample indicates the presence of said immunodeficiency virus MVP-5180/91, or variants of said virus.

52. A method of detecting the presence of an immunodeficiency virus of the HIV group which has the designation MVP-5180/91 and which has been deposited with the European Collection of Animal Cell Cultures (ECAC) under No. V 920 92 318, or variants of said virus, wherein said variants show, at least, 83% identity with SEQ ID NO:56 at the LTR gene, 71% identity with SEQ ID NO:56 at the GAG gene, 75% identity with SEQ ID NO:56 at the POL gene, 69% identity with SEQ ID NO:56 at the VIF gene, 54% identity with SEQ ID NO:56 at the ENV gene, and 84% identity with SEQ ID NO:56 at the NEF gene, wherein said method comprises: (a) combining a sample with an oligonucleotide whose sequence is present within the sequence of SEQ ID NO:56 or the complement of SEQ ID NO:56; and (b) detecting hybridization of said oligonucleotide to nucleic acid present in said sample, wherein hybridization of said oligonucleotide to nucleic acid present in said sample indicates the presence of said immunodeficiency virus MVP-5180/91, or variants of said virus.

53. The method of claim 52, wherein said variants show, at least, 85% identity with SEQ ID NO:56 at the LTR gene, 72% identity with SEQ ID NO:56 at the GAG gene, 76% identity with SEQ ID NO:56 at the POL gene, 70% identity with SEQ ID NO:56 at the VIF gene, 55% identity with SEQ ID NO:56 at the ENV gene, and 88% identity with SEQ ID NO:56 at the NEF gene.

54. The method of claim 52, wherein said variants show, at least, 90% identity with SEQ ID NO:56 at the LTR gene, 86% identity with SEQ ID NO:56 at the GAG gene, 88% identity with SEQ ID NO:56 at the POL gene,

85% identity with SEQ ID NO:56 at the VIF gene, 78% identity with SEQ ID NO:56 at the ENV gene, and 90% identity with SEQ ID NO:56 at the NEF gene.

55. An oligonucleotide of at least 17 nucleotide bases having greater than 83% homology with the LTR locus of virus MVP-5180/91.

56. The oligonucleotide of claim 55, wherein said oligonucleotide has greater than 85% homology with the LTR locus of virus MVP-5180/91.

57. The oligonucleotide of claim 56, wherein said oligonucleotide has greater than 90% homology with the LTR locus of virus MVP-5180/91.

58. The oligonucleotide of claim 55, wherein said oligonucleotide is from approximately 17 to 42 bases in length.

59. The oligonucleotide of claim 55, wherein said oligonucleotide is from approximately 20 to 25 bases in length.

60. An oligonucleotide of at least 17 nucleotide bases having greater than 71% homology with the GAG locus of virus MVP-5180/91.

61. The oligonucleotide of claim 60, wherein said oligonucleotide has greater than 72% homology with the GAG locus of virus MVP-5180/91.

62. The oligonucleotide of claim 61, wherein said oligonucleotide has greater than 86% homology with the GAG locus of virus MVP-5180/91.

63. The oligonucleotide of claim 60, wherein said oligonucleotide is from approximately 17 to 42 bases in length.

64. The oligonucleotide of claim 60, wherein said oligonucleotide is from approximately 20 to 25 bases in length.

65. An oligonucleotide of at least 17 nucleotide bases having greater than 75% homology with the POL locus of virus MVP-5180/91.

66. The oligonucleotide of claim 65, wherein said oligonucleotide has greater than 86% homology with the POL locus of virus MVP-5180/91.

67. The oligonucleotide of claim 66, wherein said oligonucleotide has greater than 88% homology with the POL locus of virus MVP-5180/91.

68. The oligonucleotide of claim 65, wherein said oligonucleotide is from approximately 17 to 42 bases in length.

69. The oligonucleotide of claim 65, wherein said oligonucleotide is from approximately 20 to 25 bases in length.

70. An oligonucleotide of at least 17 nucleotide bases having greater than 69% homology with the VIF locus of virus MVP-5180/91.

71. The oligonucleotide of claim 70, wherein said oligonucleotide has greater than 70% homology with the VIF locus of virus MVP-5180/91.

72. The oligonucleotide of claim 71, wherein said oligonucleotide has greater than 85% homology with the VIF locus of virus MVP-5180/91.

73. The oligonucleotide of claim 70, wherein said oligonucleotide is from approximately 17 to 42 bases in length.

74. The oligonucleotide of claim 70, wherein said oligonucleotide is from approximately 20 to 25 bases in length.

75. An oligonucleotide of at least 17 nucleotide bases having greater than 54% homology with the ENV locus of virus MVP-5180/91.

76. The oligonucleotide of claim 75, wherein said oligonucleotide has greater than 55% homology with the ENV locus of virus MVP-5180/91.

77. The oligonucleotide of claim 76, wherein said oligonucleotide has greater than 78% homology with the ENV locus of virus MVP-5180/91.

78. The oligonucleotide of claim 75, wherein said oligonucleotide is from approximately 17 to 42 bases in length.

79. The oligonucleotide of claim 75, wherein said oligonucleotide is from approximately 20 to 25 bases in length.

80. An oligonucleotide of at least 17 nucleotide bases having greater than 84% homology with the NEF locus of virus MVP-5180/91.

81. The oligonucleotide of claim 80, wherein said oligonucleotide has greater than 88% homology with the NEF locus of virus MVP-5180/91.

82. The oligonucleotide of claim 81, wherein said oligonucleotide has greater than 90% homology with the NEF locus of virus MVP-5180/91.

83. The oligonucleotide of claim 80, wherein said oligonucleotide is from approximately 17 to 42 bases in length.

84. The oligonucleotide of claim 80, wherein said oligonucleotide is from approximately 20 to 25 bases in length.

85. A method of detecting the presence of an immunodeficiency virus of the HIV group which has the designation MVP-5180/91 and which has been deposited with the European Collection of Animal Cell Cultures (ECAC) under No. V 920 92 318, or variants of said virus, wherein said variants have nucleic acid which shows more than 66% homology to SEQ ID NO:56, wherein said method comprises: (a) combining a sample with the oligonucleotide of claim 55; and (b) detecting hybridization of said oligonucleotide to nucleic acid present in said sample, wherein hybridization of said oligonucleotide to nucleic acid present in said sample indicates the presence of said immunodeficiency virus MVP-5180/91, or variants of said virus.

86. A method of detecting the presence of an immunodeficiency virus of the HIV group which has the designation MVP-5180/91 and which has been deposited with the European Collection of Animal Cell Cultures (ECAC) under No. V 920 92 318, or variants of said virus, wherein said variants show, at least, 83% identity with SEQ ID NO:56 at the LTR gene, 71% identity with SEQ ID NO:56 at the GAG gene, 75% identity with SEQ ID NO:56 at the POL gene, 69% identity with SEQ ID NO:56 at the VIF gene, 54% identity with SEQ ID NO:56 at the ENV gene, and 84% identity with SEQ ID NO:56 at the NEF gene, wherein said method comprises: (a) combining a sample with the oligonucleotide of claim 55; and (b) detecting hybridization of said oligonucleotide to nucleic acid present in said sample, wherein hybridization of said oligonucleotide to nucleic acid present in said sample indicates the presence of said immunodeficiency virus MVP-5180/91, or variants of said virus.

87. A method of detecting the presence of an immunodeficiency virus of the HIV group which has the designation MVP-5180/91 and which has been deposited with the European Collection of Animal Cell Cultures (ECAC) under No. V 920 92 318, or variants of said virus, wherein said variants have nucleic acid which shows more than 66% homology to SEQ ID NO:56, wherein said method comprises: (a) combining a sample with the oligonucleotide of claim 60; and (b) detecting hybridization of said oligonucleotide to nucleic acid present in said sample, wherein hybridization of said oligonucleotide to nucleic acid present in said sample indicates the presence of said immunodeficiency virus MVP-5180/91, or variants of said virus.

88. A method of detecting the presence of an immunodeficiency virus of the HIV group which has the designation MVP-5180/91 and which has been deposited with the European Collection of Animal Cell Cultures (ECAC) under No. V 920 92 318, or variants of said virus, wherein said variants show, at least, 83% identity with SEQ ID NO:56 at the LTR gene, 71% identity with SEQ ID NO:56 at the GAG gene, 75% identity with SEQ ID NO:56 at the POL gene, 69% identity with SEQ ID NO:56 at the VIF gene, 54% identity with SEQ ID NO:56 at the ENV gene, and 84% identity with SEQ ID NO:56 at the NEF gene, wherein said method comprises: (a) combining a sample with the oligonucleotide of claim 60; and (b) detecting hybridization of said oligonucleotide to nucleic acid present in said sample, wherein hybridization of said oligonucleotide to nucleic acid present in said sample indicates the presence of said immunodeficiency virus MVP-5180/91, or variants of said virus.

89. A method of detecting the presence of an immunodeficiency virus of the HIV group which has the designation MVP-5180/91 and which has been deposited with the European Collection of Animal Cell Cultures (ECAC) under No. V 920 92 318, or variants of said virus, wherein said variants have nucleic acid which shows more than 66% homology to SEQ ID NO:56, wherein said method comprises: (a) combining a sample with the oligonucleotide of claim 65; and (b) detecting hybridization of said oligonucleotide to nucleic acid present in said sample, wherein hybridization of said oligonucleotide to nucleic acid present in said sample indicates the presence of said immunodeficiency virus MVP-5180/91, or variants of said virus.

90. A method of detecting the presence of an immunodeficiency virus of the HIV group which has the designation MVP-5180/91 and which has been deposited with the European Collection of Animal Cell Cultures (ECAC) under No. V 920 92 318, or variants of said virus, wherein said variants show, at least, 83% identity with SEQ ID NO:56 at the LTR gene, 71% identity with SEQ ID NO:56 at the GAG gene, 75% identity with SEQ ID NO:56 at the POL gene, 69% identity with SEQ ID NO:56 at the VIF gene, 54% identity with SEQ ID NO:56 at the ENV gene, and 84% identity with SEQ ID NO:56 at the NEF gene, wherein said method comprises: (a) combining a sample with the oligonucleotide of claim 65; and (b) detecting hybridization of said oligonucleotide to nucleic acid present in said sample, wherein hybridization of said oligonucleotide to nucleic acid present in said sample indicates the presence of said immunodeficiency virus MVP-5180/91, or variants of said virus.

91. A method of detecting the presence of an immunodeficiency virus of the HIV group which has the designation MVP-5180/91 and which has been deposited with the European Collection of Animal Cell Cultures (ECAC) under No. V 920 92 318, or variants of said virus, wherein said variants have nucleic acid which shows more than 66% homology to SEQ ID NO:56, wherein said method comprises: (a) combining a sample with the oligonucleotide of claim 70; and (b) detecting hybridization of said oligonucleotide to nucleic acid present in said sample, wherein hybridization of said oligonucleotide to nucleic acid present in said sample indicates the presence of said immunodeficiency virus MVP-5180/91, or variants of said virus.

92. A method of detecting the presence of an immunodeficiency virus of the HIV group which has the designation MVP-5180/91 and which has been deposited with the European Collection of Animal Cell Cultures (ECAC) under No. V 920 92 318, or variants of said virus, wherein said variants show, at least, 83% identity with SEQ ID NO:56 at the LTR gene, 71% identity with SEQ ID NO:56 at the GAG gene, 75% identity with SEQ ID NO:56 at the POL gene, 69% identity with SEQ ID NO:56 at the VIF gene, 54% identity with SEQ ID NO:56 at the ENV gene, and 84% identity with SEQ ID NO:56 at the NEF gene, wherein said method comprises: (a) combining a sample with the oligonucleotide of claim 70; and (b) detecting hybridization of said oligonucleotide to nucleic acid present

in said sample, wherein hybridization of said oligonucleotide to nucleic acid present in said sample indicates the presence of said immunodeficiency virus MVP-5180/91, or variants of said virus.

93. A method of detecting the presence of an immunodeficiency virus of the HIV group which has the designation MVP-5180/91 and which has been deposited with the European Collection of Animal Cell Cultures (ECAC) under No. V 920 92 318, or variants of said virus, wherein said variants have nucleic acid which shows more than 66% homology to SEQ ID NO:56, wherein said method comprises: (a) combining a sample with the oligonucleotide of claim 75; and (b) detecting hybridization of said oligonucleotide to nucleic acid present in said sample, wherein hybridization of said oligonucleotide to nucleic acid present in said sample indicates the presence of said immunodeficiency virus MVP-5180/91, or variants of said virus.

94. A method of detecting the presence of an immunodeficiency virus of the HIV group which has the designation MVP-5180/91 and which has been deposited with the European Collection of Animal Cell Cultures (ECAC) under No. V 920 92 318, or variants of said virus, wherein said variants show, at least, 83% identity with SEQ ID NO:56 at the LTR gene, 71% identity with SEQ ID NO:56 at the GAG gene, 75% identity with SEQ ID NO:56 at the POL gene, 69% identity with SEQ ID NO:56 at the VIF gene, 54% identity with SEQ ID NO:56 at the ENV gene, and 84% identity with SEQ ID NO:56 at the NEF gene, wherein said method comprises: (a) combining a sample with the oligonucleotide of claim 75; and (b) detecting hybridization of said oligonucleotide to nucleic acid present in said sample, wherein hybridization of said oligonucleotide to nucleic acid present in said sample indicates the presence of said immunodeficiency virus MVP-5180/91, or variants of said virus.

95. A method of detecting the presence of an immunodeficiency virus of the HIV group which has the designation MVP-5180/91 and which has been deposited with the European Collection of Animal Cell Cultures (ECAC) under No. V 920 92 318, or variants of said virus, wherein said variants have nucleic acid which shows more than 66% homology to SEQ ID NO:56, wherein said method comprises: (a) combining a sample with the oligonucleotide of claim 80; and (b) detecting hybridization of said oligonucleotide to nucleic acid present in said sample, wherein hybridization of said oligonucleotide to nucleic acid present in said sample indicates the presence of said immunodeficiency virus MVP-5180/91, or variants of said virus.

96. A method of detecting the presence of an immunodeficiency virus of the HIV group which has the designation MVP-5180/91 and which has been deposited with the European Collection of Animal Cell Cultures (ECAC) under No. V 920 92 318, or variants of said virus, wherein said variants show, at least, 83% identity with SEQ ID NO:56 at the LTR gene, 71% identity with SEQ ID NO:56 at the GAG gene, 75% identity with SEQ ID NO:56 at the POL gene, 69% identity with SEQ ID NO:56 at the VIF gene, 54% identity with SEQ ID NO:56 at the ENV gene, and 84% identity with SEQ ID NO:56 at the NEF gene, wherein said method comprises: (a) combining a sample with the oligonucleotide of claim 80; and (b) detecting hybridization of said oligonucleotide to nucleic acid present in said sample, wherein hybridization of said oligonucleotide to nucleic acid present in said sample indicates the presence of said immunodeficiency virus MVP-5180/91, or variants of said virus.

L5 ANSWER 9 OF 16 USPATFULL on STN
2000:15322 Toxoplasma gondii antigens, the preparation thereof and the use thereof.
Knapp, Stefan, Marburg, Germany, Federal Republic of
Ziegelmaier, Robert, Marburg, Germany, Federal Republic of
Kupper, Hans, Marburg, Germany, Federal Republic of
Dade Behring Marburg GmbH, Marburg, Germany, Federal Republic of (non-U.S.

corporation)
US 6022546 20000208
APPLICATION: US 1994-301162 19940906 (8)
PRIORITY: DE 1989-3940598 19891208
DOCUMENT TYPE: Utility; Granted.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to the identification of Toxoplasma gondii antigens and the preparation thereof by genetic engineering. A cDNA expression gene bank of this parasite was prepared. Recombinant clones which are of diagnostic interest were identified using a high-titer rabbit anti-Toxoplasma gondii serum, and isolated.
CLM What is claimed is:
1. A substantially purified protein comprising at least one amino acid sequence consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 16, 18, or 20 and immunogenic fragments thereof, or (b) an amino acid sequence encoded by a DNA sequence of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 14, 15, 17 or 19.

2. An immunogenic composition which contains one or more proteins as claimed in claim 1.

L5 ANSWER 10 OF 16 USPATFULL on STN
1998:147203 Retrovirus from the HIV group and its use.
Guertler, Lutz G., Munich, Germany, Federal Republic of
Eberle, Josef, Freising, Germany, Federal Republic of
Brunn, Albrecht v., Augsburg, Germany, Federal Republic of
Knapp, Stefan, Marburg-Wehrshausen, Germany, Federal Republic of
Hauser, Hans-Peter, Marburg, Germany, Federal Republic of
Behring Diagnostics GmbH, Marburg, Germany, Federal Republic of (non-U.S. corporation)
US 5840480 19981124
APPLICATION: US 1995-468059 19950606 (8)
PRIORITY: DE 1992-4233646 19921006
DE 1992-4235718 19921022
DE 1992-4244541 19921230
DE 1993-4318186 19930601
DOCUMENT TYPE: Utility; Granted.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A novel immunodeficiency virus is disclosed which has the designation MVP-5180/91 (SEQ ID NO:56) and which has been deposited with the European Collection of Animal Cell Cultures (ECACC) under No. V 920 92 318. The characteristic antigens which can be obtained from it and which can be employed for detecting antibodies against retroviruses which are associated with immuno-deficiency diseases are also disclosed, as are the DNA and amino acid sequences of the virus.
CLM What is claimed is:
1. An immunodeficiency virus of the HIV group, or variants of said virus, which exhibits all the essential morphological and immunological properties of the retrovirus which has the designation MVP-5180/91 (SEQ ID NO:56) and which has been deposited with the European Collection of Animal Cell Cultures (ECACC) under No. V 920 92 318.

2. The immunodeficiency virus as claimed in claim 1, which exhibits a protein band in a Western blot indicating a reverse transcriptase, that is about 3-7 kilodaltons smaller than the corresponding band of HIV-1 and/or HIV-2 viruses.

3. The immunodeficiency virus as claimed in one of the claims 1 or 2, which retrovirus exhibits less reactivity with a monoclonal antibody directed against protein p 24, related to reverse transcriptase activity, than does the HIV-1 virus, and more activity, related to the activity of reverse transcriptase, than does HIV-2.

4. The immunodeficiency virus as claimed in claim 1, wherein antigen/antibody reactions with its transmembrane protein gp 41 are detectable using sera from patients originating from Africa, and wherein

only a relatively small antigen/antibody reaction, or no such reaction, can be detected with the gp 41 using sera from patients originating from Germany.

5. The immunodeficiency virus as claimed in claim 1, which has an RNA sequence which is homologous to about 75% or more, based on the entire genome, with the RNA of the deposited virus.

6. The immunodeficiency virus as claimed in claim 1, which has an RNA sequence which is homologous to the extent of at least 75% with the RNA sequence of SEQ ID NO:37.

7. The immunodeficiency virus as claimed in claim 1, which has a nucleotide sequence which is homologous to the extent of at least 75% with the sequence of SEQ ID NO:44, or parts thereof.

8. The immunodeficiency virus as claimed in claim 7, wherein the part of the sequence is at least 50 nucleotides long.

9. The immunodeficiency virus as claimed in claim 1, which has a sequence of FIG. 4 (SEQ ID NO:56) or is homologous to this sequence, where the differences from the sequence given in FIG. 4 (SEQ ID NO:56), related to the gene loci, are at most LTR: 17%, GAG: 29%, POL: 25%, VIF: 31%, ENV: 46%, NEF: 16%.

10. The immunodeficiency virus as claimed in claim 1, which has a sequence of FIG. 4 (SEQ ID NO:56) or is homologous to this sequence, where the differences from the sequence given in FIG. 4 (SEQ ID NO:56), related to the gene loci, are at most LTR: 10%, GAG: 14%, POL: 12%, VIF: 15%, ENV: 22%, NEF: 10%.

11. Ribonucleic acid characterized in that the ribonucleic acid is coding for an immunodeficiency virus as claimed in claim 1.

L5 ANSWER 11 OF 16 USPATFULL on STN
1998:72459 Retrovirus from the HIV group and its use.
Guertler, Lutz G., Munich, Germany, Federal Republic of
Eberle, Josef, Freising, Germany, Federal Republic of
Brunn, Albrecht V., Augsburg, Germany, Federal Republic of
Knapp, Stefan, Marburg-Wehrshausen, Germany, Federal Republic of
Hauser, Hans-Peter, Marburg, Germany, Federal Republic of
Behring Diagnostics GmbH, Marburg, Germany, Federal Republic of (non-U.S. corporation)
US 5770427 19980623
APPLICATION: US 1995-471770 19950606 (8)
PRIORITY: DE 1992-4233646 19921006
DE 1992-4235718 19921022
DE 1992-4244541 19921230
DE 1993-4318186 19930601
DOCUMENT TYPE: Utility; Granted.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A novel immunodeficiency virus is disclosed which has the designation MVP-5180/91 (SEQ ID NO:56) and which has been deposited with the European Collection of Animal Cell Cultures (ECACC) under No. V 920 92 318. The characteristic antigens which can be obtained from it and which can be employed for detecting antibodies against retroviruses which are associated with immunodeficiency diseases are also disclosed, as are the DNA and amino acid sequences of the virus.
CLM What is claimed is:
1. A cDNA which is complementary to the RNA, or parts of said RNA which encode at least 15 amino acids, of an immunodeficiency virus having all the morphological and immunological properties of retrovirus MVP-5180/91 (SEQ ID NO:56) which has been deposited with the European Collection of Animal Cell Culture (ECACC) under No. V 920 92 318, and having a sequence homology of more than 70% to the env gene of the retrovirus

MVP-5180/91.

2. A cDNA which is complementary to the RNA, or parts of said RNA which encode at least 15 amino acids, of the immunodeficiency virus MVP-5180/91 (SEQ ID NO:56) deposited with the European Collection of Animal Cell Cultures (ECACC) under NO. V 920 92 318.

L5 ANSWER 12 OF 16 USPATFULL on STN
1998:61390 Retrovirus from the HIV group and its use.
Guertler, Lutz G., Munich, Germany, Federal Republic of
Eberle, Josef, Freising, Germany, Federal Republic of
Brunn, Albrecht V., Augsburg, Germany, Federal Republic of
Knapp, Stefan, Marburg-Wehrshausen, Germany, Federal Republic of
Hauser, Hans-Peter, Marburg, Germany, Federal Republic of
Behring Diagnostics GmbH, Marburg, Germany, Federal Republic of (non-U.S. corporation)
US 5759770 19980602
APPLICATION: US 1995-470202 19950606 (8)
PRIORITY: DE 1992-4233646 19921006
DE 1992-4235718 19921022
DE 1992-4244541 19921230
DE 1993-4318186 19930601
DOCUMENT TYPE: Utility; Granted.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A novel immunodeficiency virus is disclosed which has the designation MVP-5180/91 (SEQ ID NO:56) and which has been deposited with the European Collection of Animal Cell Cultures (ECACC) under No. V 920 92 318. The characteristic antigens which can be obtained from it and which can be employed for detecting antibodies against retroviruses which are associated with immunodeficiency diseases are also disclosed, as are the DNA and amino acid sequences of the virus.
CLM What is claimed is:
1. An antigen comprising a peptide encoded by cDNA that is complementary to the RNA of an immunodeficiency virus having all the morphological and immunological properties of retrovirus MVP-5180/91 which has been deposited with the European Collection of Animal Cell Culture (ECACC) under No. V 920 92 318, and having a sequence identity of more than 70% to the env gene of the retrovirus MVP-5180/91.

2. The antigen as claimed in claim 1, which comprises the amino acid sequence of SEQ ID NO:46 or an antigenic portion thereof.

3. The antigen as claimed in claim 1, which comprises the amino acid sequence of SEQ ID NO:46.

4. The antigen as claimed in claim 2, which comprises the amino acid sequence of SEQ ID NO:62, or an antigenic portion thereof.

5. The antigen as claimed in claim 2, which comprises the amino acid sequence of SEQ ID NO:62.

6. An antigen comprising a peptide encoded by cDNA that is complementary to the RNA of retrovirus MVP-5180/91 which has been deposited with the European Collection of Animal Cell Culture (ECACC) under No. V 920 92 318.

7. The antigen as claimed in claim 6, which comprises the amino acid sequence of SEQ ID NO:46.

8. The antigen as claimed in claim 6, which comprises the amino acid sequence of SEQ ID NO:62.

9. A test kit for detecting antibodies against viruses that cause immunodeficiency comprising the antigen of claim 1 and ancillary reagents suitable for use in detecting the presence of antibodies to the

antigen in a biological sample.

10. The test kit as claimed in claim 9, in which the antigen comprises an amino acid sequence of SEQ ID NO:46.

11. The test kit as claimed in claim 9, in which the antigen comprises an amino acid sequence of SEQ ID NO:62.

12. The test kit as claimed in claim 9, which is a Western blot.

13. The test kit as claimed in claim 9, which is an ELISA test or a fluorescence-antibody detection test.

14. An assay for the detection of antibodies against viruses that cause immunodeficiency comprising the steps of: (i) contacting the antigen as claimed in claim 1 with a biological sample from a patient suspected of being infected with a virus causing immunodeficiency; and (ii) detecting the presence or absence of a complex formed between the antigen and antibodies specific therefor present in the sample.

15. The assay as claimed in claim 14, in which the antigen is coated on a surface.

16. An assay for the detection of antibodies against viruses that cause immunodeficiency comprising the steps of: (i) contacting the antigen as claimed in claim 6 with a biological sample from a patient suspected of being infected with a virus causing immunodeficiency; and (ii) detecting the presence or absence of a complex formed between the antigen and antibodies specific therefor present in the sample.

17. An antigenic composition comprising the antigen as claimed in claim 1.

18. An antigenic composition comprising the antigen as claimed in claim 6.

19. The antigen as claimed in claim 1 produced by recombinant methods.

20. The antigen as claimed in claim 1 produced by synthetic methods.

L5 ANSWER 13 OF 16 USPATFULL on STN
96:111348 Nucleic acid encoding a signal peptide, a recombinant molecule comprising the nucleic acid, methods of using the nucleic acid, and methods of using the signal peptide.
Knapp, Stefan, Marburg, Germany, Federal Republic of
Amann, Egon, Marburg, Germany, Federal Republic of
Abel, Karl-Josef, Marburg, Germany, Federal Republic of
Behringwerke Aktiengesellschaft, Marburg, Germany, Federal Republic of (non-U.S. corporation)
US 5580758 19961203
APPLICATION: US 1995-385366 19950207 (8)
PRIORITY: DE 1989-3901681 19890121
DOCUMENT TYPE: Utility; Granted.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention relates to a nucleic acid encoding a signal peptide from Bordetella pertussis, a recombinant molecule comprising the signal peptide, and processes for optimizing protein expression in Gram-negative bacteria employing the nucleic acid or signal peptide.
CLM What is claimed is:
1. An isolated nucleic acid encoding a signal peptide from Bordetella pertussis, wherein said signal peptide has the following amino acid sequence: MKKWFVAAGIGAAGLMLSSAA.

2. A recombinant molecule comprising a nucleic acid encoding a signal peptide from Bordetella pertussis as claimed in claim 1.

3. A process for secreting proteins in gram-negative bacteria comprising: 1) inserting a nucleic acid encoding a signal peptide as set forth in claim 2 in front of a structural gene encoding a protein to be expressed thereby generating a construct in which said signal peptide directs the secretion of said protein; and 2) expressing said construct in a gram-negative bacteria such that said protein is secreted.

L5 ANSWER 14 OF 16 USPATFULL on STN
95:102732 Electromagnetically actuated valve.
Sausner, Andreas, Neu Isenburg, Germany, Federal Republic of
Knapp, Stefan, Waldmichelbach, Germany, Federal Republic of
Firma Carl Freudenberg, Weinheim, Germany, Federal Republic of (non-U.S. corporation)
US 5467961 19951121
APPLICATION: US 1994-239082 19940506 (8)
PRIORITY: DE 1993-4315013 19930506
DOCUMENT TYPE: Utility; Granted.

AB An electromagnetically actuated valve comprising an annular-shaped solenoid coil arranged in a housing and surrounding an axially reciprocal magnet armature of metallic material is disclosed. The magnet armature is provided on a front end with an elastomeric sealing member facing a valve seat made of elastomeric material. The magnet armature and the sealing member are joined together via form locking.

CLM What is claimed is:

1. An electromagnetically actuated valve, comprising: a valve housing; a metallic magnet armature having a first end and a second end and an axially extending through-bore penetrating therethrough, the through bore being completely filled by an elastomeric material which extend through the first end to provide a stop buffer on the first end of the magnet armature and through the second end to provide an elastomeric sealing member on the second end of the magnet armature that is form-lockingly joined to the magnet armature via a grooved undercut that extends on the periphery of the magnet armature, said undercut and said sealing member being in engagement with one another; at least one annularly-shaped solenoid coil that is arranged within the valve housing and which, along a portion of its interior annulus, surrounds the magnet armature, said magnet armature being capable of axially reciprocal motion with respect to the solenoid coil; and a valve seat, against which the sealing member of the magnet armature may selectively be brought into operative engagement.

2. The electromagnetically actuated valve according to claim 1, wherein the magnet armature is provided with cavities having a depth of 0.5 mm to 3.0 mm.

3. The electromagnetically actuated valve according to claim 1, wherein the magnet armature is provided with cavities having a depth of 0.5 mm to 3.0 mm.

4. The electromagnetically actuated valve according to claim 1, wherein in the area of the through-bore the magnet armature has an internal screw thread.

5. The electromagnetically actuated valve according to claim 1, wherein the cross section of the through-bore is step-wise reduced in area in the direction of the sealing member.

6. The electromagnetically actuated valve according to claim 1, wherein the elastomeric material of the sealing member has a Shore hardness A of 40 to 100.

7. An electromagnetically actuated valve, comprising: a valve housing; a metallic magnet armature having a first end and a second end, the second end having an elastomeric sealing member that is form-lockingly joined

to the magnet armature, wherein the magnet armature is penetrated by an axially extending through-bore that conically widens from the second end to the first end, said through-bore being completely filled by the elastomeric material of the sealing member, and wherein the elastomeric material forms a stop buffer on the first end of said magnet armature; at least one annularly-shaped solenoid coil that is arranged within the valve housing and which, along a portion of its interior annulus, surrounds the magnet armature, said magnet armature being capable of axially reciprocal motion with respect to the solenoid coil; and a valve seat, against which the sealing member of the magnet armature may selectively be brought into operative engagement.

8. The electromagnetically actuated valve according to claim 7, wherein the through-bore conically widens at an angle of between 2 and 45 degrees with respect to the central longitudinal axis of the through-bore.

9. The electromagnetically actuated valve according to claim 7, wherein the through-bore conically widens at an angle of between 5 and 30 degrees with respect to the central longitudinal axis of the through-bore.

L5 ANSWER 15 OF 16 USPATFULL on STN

95:59443 Device for feeding vapors of a fuel tank into an internal combustion engine.

Wojts-Saary, Jurgen, Reinheim, Germany, Federal Republic of
Heinemann, Joachim, Weinheim, Germany, Federal Republic of
Tinz, Reinhard, Gross-Biberau, Germany, Federal Republic of
Knapp, Stefan, Waldmichelbach, Germany, Federal Republic of
Firma Carl Freudenberg, Weinheim, Germany, Federal Republic of (non-U.S. corporation)

US 5429097 19950704
APPLICATION: US 1993-160998 19931203 (8)
PRIORITY: DE 1992-42412749 19921208
DOCUMENT TYPE: Utility; Granted.

AB A device for feeding the vapors present in the free space of a fuel tank into the intake manifold of an internal combustion engine wherein the free space and the intake manifold are connected by a line in which an activated carbon container and a stop valve are connected in series, the activated carbon container being connected with the atmosphere by a vent line and the vent line can be closed by a vent line valve. The device further comprises an excess pressure valve and/or a vacuum valve which may be in the same housing as the vent line valve.

CLM What is claimed is:

1. A device for feeding vapors present in a free space of a fuel tank into an intake manifold of an internal combustion engine wherein the free space and the intake manifold are connected by a line in which an activated carbon container and a stop valve are arranged in series, the activated carbon container being connected with the atmosphere by a vent line, and further comprising: a vent line valve for selectively opening and closing the vent line which connects the activated carbon container to the atmosphere; an excess pressure valve for providing an opening to the atmosphere upon exceeding a maximum pressure; and a vacuum valve for providing an opening to the atmosphere upon falling below a minimum pressure; wherein the vent line valve, the excess pressure valve and the vacuum valve are combined in a housing.

2. A device according to claim 1 wherein the vent line valve, the excess pressure valve and the vacuum valve have closure elements which are moveable independently of each other and which have one continuous axis of movement.

3. A device according to claim 2 wherein the closure element of the excess pressure valve comprises elastomeric material, is developed as a shuttle valve, and is attached as one continuous piece to the closure

element of the vacuum valve.

4. A device according to claim 2 wherein the closure element of the vent line valve can be brought into a closed position by an electromagnet against the force of a compression spring.

5. A device according to claim 4 wherein the compression spring is arranged on a side of the closure element of the vent line valve facing away from the electromagnet.

6. A device according to claim 4 wherein the closure element of the vent line valve is sealed off from the housing by a diaphragm.

7. A device according to claim 4 wherein the compression spring is supported on the closure element of the vacuum valve.

8. A device according to claim 7 wherein the closure element of the vacuum valve is guided by a column-shaped projection formed integrally with the closure element of the vacuum valve and engaging into the compression spring.

9. A device according to claim 4 wherein the compression spring is surrounded on the outside by a guide tube connected to the housing and wherein the compression spring is guided by the guide tube.

10. A device according to claim 1 wherein the excess pressure valve and the vacuum valve are located along the line between the stop valve and the fuel tank.

11. A device according to claim 10 wherein the excess pressure valve and the vacuum valve are located along the vent line between the vent line valve and the activated carbon container.

12. A device for feeding vapors present in a free space of a fuel tank into an intake manifold of an internal combustion engine wherein the free space and the intake manifold are connected by a line in which an activated carbon container and a stop valve are arranged in series, the activated carbon container being connected with the atmosphere by a vent line, and further comprising: a vent line valve for selectively opening and closing the vent line which connects the activated carbon container to the atmosphere; and an excess pressure valve for providing an opening to the atmosphere upon exceeding a maximum pressure; wherein the vent line valve and the excess pressure valve are combined in a housing.

13. A device according to claim 12 wherein the vent line valve and the excess pressure valve have closure elements which are moveable independently of each other and which have one continuous axis of movement.

14. A device according to claim 13 wherein the closure element of the excess pressure valve comprises elastomeric material and is developed as a shuttle valve.

15. A device according to claim 13 wherein the closure element of the vent line valve can be brought into a closed position by an electromagnet against the force of a compression spring.

16. A device according to claim 15 wherein the closure element of the vent line valve is sealed off from the housing by a diaphragm.

17. A device for feeding vapors present in a free space of a fuel tank into an intake manifold of an internal combustion engine wherein the free space and the intake manifold are connected by a line in which an activated carbon container and a stop valve are arranged in series, the activated carbon container being connected with the atmosphere by a vent line, and further comprising: a vent line valve for selectively opening

and closing the vent line which connects the activated carbon container to the atmosphere; and a vacuum valve for providing an opening to the atmosphere upon falling below a minimum pressure; wherein the vent line valve and the vacuum valve are combined in a housing.

18. A device according to claim 17 wherein the vent line valve and the vacuum valve have closure elements which are moveable independently of each other and which have one continuous axis of movement.

19. A device according to claim 18 wherein the closure element of the vent line valve can be brought into a closed position by an electromagnet against the force of a compression spring.

20. A device according to claim 19 wherein the closure element of the vent line valve is sealed off from the housing by a diaphragm.

L5 ANSWER 16 OF 16 USPATFULL on STN
92:89171 Signal peptide for the secretion of peptides in Escherichia coli.
Knapp, Stefan, Marburg, Germany, Federal Republic of
Amann, Egon, Marburg, Germany, Federal Republic of
Abel, Karl-Josef, Marburg, Germany, Federal Republic of
Behringwerde Aktiengesellschaft, Marburg, Germany, Federal Republic of (non-U.S. corporation)
US 5159062 19921027
APPLICATION: US 1990-467551 19900119 (7)
PRIORITY: DE 1989-3901681 19890121
DOCUMENT TYPE: Utility; Granted.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention relates to a new signal peptide from Bordetella pertussis with the amino acid sequence M K K W F V A A G I G A G L L M L S S A A and to particularly suitable expression vectors with whose aid such signal sequences can be found and/or evaluated.
CLM What is claimed is:
1. A fusion peptide consisting of a signal peptide from Bordetella pertussis fused to a heterologous protein, wherein said signal peptide has the following amino acid sequence: ##STR20##

=> d l5,cbib,exnam,8

L5 ANSWER 8 OF 16 USPATFULL on STN
2001:136366 Diagnostic assay for detection of HIV.
Guertler, Lutz G., Munich, Germany, Federal Republic of
Eberle, Josef, Freising, Germany, Federal Republic of
Brunn, Albrecht v., Augsburg, Germany, Federal Republic of
Knapp, Stefan, Marburg-Wehrshausen, Germany, Federal Republic of
Hauser, Hans-Peter, Marburg, Germany, Federal Republic of
Dade Behring Marburg GmbH, Marburg, Germany, Federal Republic of (non-U.S. corporation)
US 6277561 B1 20010821
APPLICATION: US 1998-109916 19980702 (9)
PRIORITY: DE 1992-4233646 19921006
DE 1992-4235718 19921022
DE 1992-4244541 19921230
DE 1993-4318186 19930601
DOCUMENT TYPE: Utility; GRANTED.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
EXNAM Primary Examiner: Park, Hankyel T.

=> e gerken manfred/in
E1 1 GERKEN KURT S/IN
E2 1 GERKEN LLL JOHN KENYON/IN
E3 10 --> GERKEN MANFRED/IN

```
E4            1      GERKEN MARK A/IN
E5            2      GERKEN MARTINA/IN
E6            1      GERKEN MICHAEL T/IN
E7            1      GERKEN MICHAEL THOMAS/IN
E8            1      GERKEN RALPH F/IN
E9            1      GERKEN ROLAND J/IN
E10           1      GERKEN ROMAN/IN
E11          16      GERKEN RUDOLF/IN
E12           2      GERKEN STEVEN L/IN

=> s e3
L6           10 "GERKEN MANFRED"/IN

=> d his

     (FILE 'HOME' ENTERED AT 20:50:07 ON 19 FEB 2004)

     FILE 'USPATFULL' ENTERED AT 20:50:23 ON 19 FEB 2004

     FILE 'USPATFULL' ENTERED AT 20:50:50 ON 19 FEB 2004
                E BRUST STEFAN/IN
L1            13 S E3
L2             0 S 6335158/PN
L3             1 S US6335158/PN
                E KNAPP STEFAN/IN
L4            24 S E3
L5            16 S L4 NOT L1
                E GERKEN MANFRED/IN
L6            10 S E3

=> s l6 not (l1 or l4)
L7             7 L6 NOT (L1 OR L4)

=> d l7,ti,1-7

L7   ANSWER 1 OF 7  USPATFULL on STN
TI     Mercaptoacetylamide derivatives, a process for their preparation and
       their use

L7   ANSWER 2 OF 7  USPATFULL on STN
TI     Preparation having increased in vivo tolerability

L7   ANSWER 3 OF 7  USPATFULL on STN
TI     Prodrugs for the therapy of tumors and inflammatory disorders

L7   ANSWER 4 OF 7  USPATFULL on STN
TI     Semisynthetic diastereomerically pure N-glycidylanthracyclines, a
       process for the stereoselective preparation thereof as the use thereof
       as cytostatics

L7   ANSWER 5 OF 7  USPATFULL on STN
TI     Glycosylated prodrugs, their method of preparation and their uses

L7   ANSWER 6 OF 7  USPATFULL on STN
TI     Anthracycline derivatives having cytostatic activity

L7   ANSWER 7 OF 7  USPATFULL on STN
TI     Anthracycline derivatives having cytostatic activity


=> d his

     (FILE 'HOME' ENTERED AT 20:50:07 ON 19 FEB 2004)

     FILE 'USPATFULL' ENTERED AT 20:50:23 ON 19 FEB 2004
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     FILE 'USPATFULL' ENTERED AT 20:50:50 ON 19 FEB 2004
                E BRUST STEFAN/IN
L1           13 S E3
L2            0 S 6335158/PN
L3            1 S US6335158/PN
                E KNAPP STEFAN/IN
L4           24 S E3
L5           16 S L4 NOT L1
                E GERKEN MANFRED/IN
L6           10 S E3
L7            7 S L6 NOT (L1 OR L4)

=> s (HIV or human immunodeficiency virus)
         29336 HIV
        372979 HUMAN
         16965 IMMUNODEFICIENCY
         70100 VIRUS
         12163 HUMAN IMMUNODEFICIENCY VIRUS
                 (HUMAN(W)IMMUNODEFICIENCY(W)VIRUS)
L8       30918 (HIV OR HUMAN IMMUNODEFICIENCY VIRUS)

=> s l8 and (MVP?)
          1059 MVP?
L9         106 L8 AND (MVP?)

=> s l9 and (MVP5180?)
            27 MVP5180?
L10         27 L9 AND (MVP5180?)

=> s l10 not (l1 or l4 or l6)
L11         21 L10 NOT (L1 OR L4 OR L6)

=> d l11,ti,1-21

L11  ANSWER 1 OF 21  USPATFULL on STN
TI     Methods and systems for producing recombinant viral antigens

L11  ANSWER 2 OF 21  USPATFULL on STN
TI     Nucleic acid mediated disruption of HIV fusogenic peptide interactions

L11  ANSWER 3 OF 21  USPATFULL on STN
TI     HIV-1 group O antigens and uses thereof

L11  ANSWER 4 OF 21  USPATFULL on STN
TI     Lentivirus from the group of immunodeficiency viruses of drill monkeys
       (Mandrillus leucophaeus) and their use

L11  ANSWER 5 OF 21  USPATFULL on STN
TI     Detection of HIV-1 by nucleic acid amplification

L11  ANSWER 6 OF 21  USPATFULL on STN
TI     RNA interference mediated inhibition of HIV gene expression using
       short interfering RNA

L11  ANSWER 7 OF 21  USPATFULL on STN
TI     Complete genome sequence of a simian immunodeficiency virus from a
       red-capped mangabey

L11  ANSWER 8 OF 21  USPATFULL on STN
TI     Non-M, non-O HIV-1 strains, fragments and uses

L11  ANSWER 9 OF 21  USPATFULL on STN
TI     Enzymatic nucleic acid treatment of diseases or conditions related to
       levels of HIV

L11  ANSWER 10 OF 21  USPATFULL on STN
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TI Lentivirus from the group of immunodeficiency viruses of drill monkeys (Mandrillus leucophaeus) and their use

L11 ANSWER 11 OF 21 USPATFULL on STN
TI Nucleotide sequences of **HIV**-1 group (or subgroup) O retroviral antigens

L11 ANSWER 12 OF 21 USPATFULL on STN
TI Complete genome sequence of a simian immunodeficiency virus from a red-capped mangabey

L11 ANSWER 13 OF 21 USPATFULL on STN
TI **HIV**-1 group O antigens and uses thereof

L11 ANSWER 14 OF 21 USPATFULL on STN
TI Non-M non-O **HIV** strains, fragments and uses

L11 ANSWER 15 OF 21 USPATFULL on STN
TI Nucleotide sequences of **HIV**-1 type (or subtype) O retrovirus antigens

L11 ANSWER 16 OF 21 USPATFULL on STN
TI Anti-**HIV** peptides and proteins

L11 ANSWER 17 OF 21 USPATFULL on STN
TI Group O **HIV**-1, fragments of such viruses, and uses thereof

L11 ANSWER 18 OF 21 USPATFULL on STN
TI Peptides for the detection of **HIV**-1 group O

L11 ANSWER 19 OF 21 USPATFULL on STN
TI Group O **HIV**-1, fragments of such viruses, and uses thereof

L11 ANSWER 20 OF 21 USPATFULL on STN
TI Methods for sensitive detection of reverse transcriptase

L11 ANSWER 21 OF 21 USPATFULL on STN
TI Oliconucleotide primers and probes for the detection of **HIV**-1

=> d l11,cbib,ab,clm,1-21

L11 ANSWER 1 OF 21 USPATFULL on STN
2004:41347 Methods and systems for producing recombinant viral antigens.
Zebedee, Suzanne, Carlsbad, CA, United States
Inchauspe, Genevieve, Lyons, FRANCE
Nasoff, Marc S., San Diego, CA, United States
Prince, Alfred S., Pound Ridge, NY, United States
Helting, Torsten B., P.O. Box 880963, San Francisco, CA, United States 94188
Nunn, Michael F., Washington, DC, United States
New York Blood Center, New York, NY, United States (U.S. corporation) by said Genevieve Inchauspe and Alfred PrinceHelting, Torsten B., San Francisco, CA, United States (U.S. individual)
US 6692751 B1 20040217
APPLICATION: US 1997-931855 19970916 (8)
DOCUMENT TYPE: Utility; GRANTED.

AB The present invention relates to recombinant expression vectors which express segments of deoxyribonucleic acid that encode recombinant **HIV** and HCV antigens. These recombinant expression vectors are transformed into host cells and used in a method to express large quantities of these antigens. The invention also provides compositions containing certain of the isolated antigens., diagnostic systems containing these antigens and methods of assaying body fluids to detect the presence of antibodies against the antigens of the invention.

CLM What is claimed is:
1. A recombinant DNA molecule comprising a vector having a procaryotic promoter operatively linked to a DNA segment, said DNA segment composed

of a first nucleotide base sequence operatively linked in frame at its 3' terminus to the 5' terminus of a second nucleotide base sequence, said first sequence having a nucleotide base sequence represented by the formula: AGGAGGGTTTTTCAT, corresponding to nucleotides 1-15 of SEQ ID NO.: 1, and said second sequence consists of a nucleotide sequence encoding amino acids 1-120 of the HCV capsid antigen.

2. The vector of claim 1, wherein said vector is pGEX7 comprising said first nucleic and second nucleic acids.

3. The vector of claim 1, wherein said amino acids are amino acids 1-120 of SEQ ID NO:8.

4. The vector of claim 3, wherein said vector is pGEX-C120H-V68.

5. The vector of claim 1, wherein said amino acids are amino acids 1-120 of SEQ ID NO:10.

6. The vector of claim 5, wherein said vector is said vector is pGEX-C120H.

7. The vector of claim 1, wherein said amino acids are amino acids 1-120 of SEQ ID NO:12.

8. The vector of claim 7, wherein said vector is pGEX-C120H-ISO2.

9. The vector of claim 1, wherein said amino acids are amino acids 1-120 of SEQ ID NO:14.

10. The vector of claim 9, wherein said vector is pGEX-C120H-ISO3.

11. A procaryotic host cell comprising an expression vector of any one of claims 1, 3, 5, 7 or 9.

12. A method of producing an HCV capsid antigen consisting of amino acid residues 1-120 which comprises: (a) treating a host cell comprising an expression vector of any one of claims 1, 3, 5, 7 and 9 under conditions and for a time effective to express said antigen; and (b) recovering said antigen from the fermentation broth following expression by using standard biochemical isolation techniques involving (i) harvest of the bacterial culture (ii) disruption of isolated cell paste (iii) differential extraction and centrifigutation of disrupted cells (iv) gel sizing and cationic exchange chromatography steps to separate the HCV capsid antigen from contaminating materials and (v) collecting the purified HCV antigen for its designated use.

13. A recombinant HCV capsid antigen produced by the method of claim 12.

14. A composition comprising a recombinant HCV capsid antigen of claim 13, wherein said composition is essentially free of procaryotic antigens and other HCV-related proteins.

L11 ANSWER 2 OF 21 USPATFULL on STN
2004:7795 Nucleic acid mediated disruption of **HIV** fusogenic peptide interactions.
Macejak, Dennis, Arvada, CO, UNITED STATES
Blatt, Lawrence, San Francisco, CA, UNITED STATES
McSwiggen, James, Boulder, CO, UNITED STATES
US 2004006035 A1 20040108
APPLICATION: US 2003-420194 A1 20030422 (10)
PRIORITY: US 2002-398036P 20020723 (60)
US 2002-374722P 20020423 (60)
US 2002-358580P 20020220 (60)
US 2002-363124P 20020311 (60)
US 2002-386782P 20020606 (60)

US 2002-406784P 20020829 (60)
US 2002-408378P 20020905 (60)
US 2002-409293P 20020909 (60)
US 2003-440129P 20030115 (60)
US 2001-294140P 20010529 (60)
DOCUMENT TYPE: Utility; APPLICATION.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The present invention relates to nucleic acid aptamers that bind to **HIV** envelope glycoprotein, gp120 and/or gp41 and methods for their use alone or in combination with other therapies, such as **HIV** RT inhibitors and **HIV** protease inhibitors. Also disclosed are nucleic acids such as siRNA, antisense, and enzymatic nucleic acid molecules that can modulate the expression of **HIV** env genes and **HIV** viral replication. The compounds and methods of the invention are expected to inhibit **HIV** viral fusion, cell entry, gene expression, and replication.

CLM What is claimed is:

1. A short interfering RNA (siRNA) molecule that down-regulates expression of a **HIV** envelope glycoprotein (env) gene by RNA interference.

2. The siRNA molecule of claim 1, wherein said **HIV** envelope glycoprotein gene encodes sequence comprising Genbank Accession number NC_-001802.

3. The siRNA molecule of claim 1, wherein the siRNA molecule comprises sequence complementary to a nucleic acid sequence encoding **HIV** envelope glycoprotein or a portion thereof.

4. The siRNA molecule of claim 1, wherein said siRNA molecule comprises about 21 nucleotides.

5. The siRNA molecule of claim 1, wherein said siRNA molecule is double stranded.

6. The siRNA molecule of claim 5, wherein each strand of said siRNA molecule comprises about 21 nucleotides.

7. The siRNA molecule of claim 1, wherein said siRNA molecule has anti-fusogenic activity against **HIV** entry into a cell.

8. The siRNA molecule of claim 1, wherein said siRNA molecule is chemically synthesized.

9. The siRNA molecule of claim 1, wherein said siRNA molecule comprises at least one nucleic acid sugar modification.

10. The siRNA molecule of claim 1, wherein said siRNA molecule comprises at least one nucleic acid base modification.

11. The siRNA molecule of claim 1, wherein said siRNA molecule comprises at least one nucleic acid backbone modification.

12. A method for modulating **HIV** cell fusion activity in a cell comprising administering to said cell the siRNA molecule of claim 1 under conditions suitable for modulating said **HIV** cell fusion activity.

13. The method of claim 12, wherein said cell is a mammalian cell.

14. The method of claim 13, wherein said mammalian cell is a human cell.

15. A method of treating **HIV**-1 infection in a subject comprising administering to the subject the siRNA of claim 1 under conditions suitable for said treatment.

16. The method of claim 15, wherein said administration is in the presence of a delivery reagent.

17. The method of claim 16, wherein said delivery reagent is a lipid.

18. The method of claim 17, wherein said lipid is a cationic lipid.

19. The method of claim 16, wherein said delivery reagent is a liposome.

20. A composition comprising the siRNA of claim 1 and a pharmaceutically acceptable carrier or diluent.

L11 ANSWER 3 OF 21 USPATFULL on STN
2003:257708 **HIV**-1 group O antigens and uses thereof.
Delaporte, Eric, Saint Jean de Cuculles, FRANCE
Peeters, Martine, Saint Jean de Cuculles, FRANCE
Saman, Eric, Bornem, BELGIUM
Vanden Haesevelde, Marleen, Oudenaarde, BELGIUM
INNOGENETICS N.V. (non-U.S. corporation)
US 2003180759 A1 20030925
APPLICATION: US 2002-320786 A1 20021216 (10)
PRIORITY: EP 1997-870110 19970718
DOCUMENT TYPE: Utility; APPLICATION.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The current invention relates to new **HIV**-1 group O antigens, nucleic acids encoding them, and the use of said antigens and/or nucleic acids as reagents in the diagnosis and prophylaxis of AIDS. It also relates to new **HIV**-1 group O strains comprising these antigens.
CLM What is claimed is:
1. Antigen derived from the gp160 env precursor protein of a new **HIV**-1 group O strain comprising at least one amino acid sequence chosen from the following group of sequences:

VQQMKI, (SEQ ID NO 53)

KIGPMSWYSMG, (SEQ ID NO 54)

MGLEKN, (SEQ ID NO 55)

IQQMKI, (SEQ ID NO 56)

KIGPLAWYSMG, (SEQ ID NO 57)

MGLERN, (SEQ ID NO 58)

QSVQEIKI, (SEQ ID NO 59)

KIGPMAWYSIG, (SEQ ID NO 60)

IGIGTT, (SEQ ID NO 61)

VQEIQT, (SEQ ID NO 62)

QTGPMAWYSIH, (SEQ ID NO 63)

IHLRTP, (SEQ ID NO 64)

IQEIKI, (SEQ ID NO 65)

KIGPMSWYSMG, (SEQ ID NO 66)

MGIGQE, (SEQ ID NO 67)

SVQELRI, (SEQ ID NO 68)

RIGPMAWYSMT, (SEQ ID NO 69)

MTLERD, (SEQ ID NO 70)

SVQEIPI, (SEQ ID NO 136) and/or at least one amino acid sequence chosen from the following group of sequences:

RNQQLLNLWGCKGRLIC, (SEQ ID NO 71)

CKGRLICYTSVQWNM, (SEQ ID NO 72)

LWGCKGRIVC, (SEQ ID NO 73)

SLWGCKGKLIC, (SEQ ID NO 74)

CKGKSIC, (SEQ ID NO 75)

CKGKIVC, (SEQ ID NO 76)

CRGRQVC, (SEQ ID NO 77)

CKGRLICYTSVH, (SEQ ID NO 79)

CKGNLIC, (SEQ ID NO 80)

CKGKMIC, (SEQ ID NO 81)

CKGRVVC, (SEQ ID NO 82) or a fragment of said antigen, said fragment consisting of at least 8, preferably 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 50 up to the maximum number of contiguous amino acids of the amino acid sequence of said antigen, with said fragment being characterized by the fact that it specifically reacts with antibodies raised against said antigen.

2. Antigen according to claim 1, characterized by an amino acid sequence comprising at least one of the following amino acid sequences:

(SEQ ID NO 83)
CERPGNNSIQQMKIGPLAWYSMGLERNKSSISRLAYC,

(SEQ ID NO 84)
CERPGNNSIQQMKIGPMAWYSMGLERNKSSISRLAYC,

(SEQ ID NO 85)
CERPGNQSVQEIKIGPMAWYSIGIGTTPANWSRIAYC,

(SEQ ID NO 86)
CERPGNQSVQEIKIGPMAWYSIGIGTTPTYNWSRIAYC,

(SEQ ID NO 87)
CVRPWNQTVQEIQTGPMAWYSIHLRTPLANLSRIAYC,

(SEQ ID NO 88)
CQRPGNLTIQEIKIGPMSWYSMGIGQEDHSKSRNAYC,

(SEQ ID NO 89)
CERPYYQSVQELRIGPMAWYSMTLERDRAGSDIRAAYC,

(SEQ ID NO 90)
CERPGNHTVQQMKIGPMSWYSMGLEKNNTSSRRAFC,

(SEQ ID NO 135)
CERTWNQSVQEIPIGPMAWYSMSVELDLNTTGSRSADC, and/or at least one amino acid sequence chosen from the following group of sequences:

DQQLLNLWGCKGRIVCYTSVKWN, (SEQ ID NO 91)

NQQLLNLWGCKGRLVCYTSVKWNK, (SEQ ID NO 92)

NQQLLNLWGCKGRLVCYTSVKWNN, (SEQ ID NO 138)

NQQRLNLWGCKGKMICYTSVPWN, (SEQ ID NO 93)

NQQLLNLWGCKGKSICYTSVKWN, (SEQ ID NO 94)

NQQLLNLWGCKGRLICYTSVQWN, (SEQ ID NO 95)

NQQRLNLWGCKGKMICYTSVKWN, (SEQ ID NO 96)

NQQLLNLWGCKGNLICYTSVKWN, (SEQ ID NO 97)

NQQLLNLWGCRGRQVCYTSVIWN, (SEQ ID NO 98)

SQQLLNLWGCKGRLICYTSVHWN, (SEQ ID NO 99)

NQQLLNLWGCKGRIVCYTSVKWN, (SEQ ID NO 100)

NQQLLNSWGCKGKIVCYTAVKWN, (SEQ ID NO 101)

NQQLLSLWGCKGKLICYTSVKWN, (SEQ ID NO 102)

NQQLLNLWGCKGRLVCYTSVQWN, (SEQ ID NO 137) or a fragment of said antigen, said fragment consisting of at least 8, preferably 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 50 up to the maximum number of contiguous amino acids of the amino acid sequence of said antigen, with said fragment being characterized by the fact that it specifically reacts with antibodies raised against said antigen.

3. Antigen according to any of claims 1 to 2, characterized by an amino acid sequence comprising at least one of the amino acid sequences represented by SEQ ID NO 2, SEQ ID NO 4, SEQ ID NO 6, SEQ ID NO 8, SEQ ID NO 10, SEQ ID NO 12, SEQ ID NO 14, SEQ ID NO 16, SEQ ID NO 18, SEQ ID NO 20, SEQ ID NO 22, SEQ ID NO 24, SEQ ID NO 26, SEQ ID NO 28, SEQ ID NO 30, SEQ ID NO 32, SEQ ID NO 34, SEQ ID NO 36, SEQ ID NO 38, SEQ ID NO 40 as shown in the alignment on FIG. 1, and/or at least one of the amino acid sequences represented by SEQ ID NO 42, SEQ ID NO 44, SEQ ID NO 46, SEQ ID NO 48, SEQ ID NO 50, or SEQ ID NO 52 as shown in the alignment on FIG. 2, and/or the amino acid sequence represented by SEQ ID NO 134, or a fragment of said antigen, said fragment consisting of at least 8, preferably 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 50 up to the maximum number of contiguous amino acids of any of the sequences represented by SEQ ID NO 2, SEQ ID NO 4, SEQ ID NO 6, SEQ ID NO 8, SEQ ID NO 10, SEQ ID NO 12, SEQ ID NO 14, SEQ ID NO 16, SEQ ID NO 18, SEQ ID NO 20, SEQ ID NO 22, SEQ ID NO 24, SEQ ID NO 26, SEQ ID NO 28, SEQ ID NO 30, SEQ ID NO 32, SEQ ID NO 34, SEQ ID NO 36, SEQ ID NO 38, SEQ ID NO 40, SEQ ID NO 42, SEQ ID NO 44, SEQ ID NO 46, SEQ ID NO 48, SEQ ID NO 50, SEQ ID NO 52, or SEQ ID NO 134 with said antigen fragment being characterized by the fact that it specifically reacts with antibodies raised against the antigen from which it is derived.

4. A polynucleic acid encoding an antigen according to any of claims 1 to 3, and more particularly a polynucleic acid comprising a nucleotide sequence chosen from the group of (I) a nucleotide sequence represented by SEQ ID NO 1, SEQ ID NO 3, SEQ ID NO 5, SEQ ID NO 7, SEQ ID NO 9, SEQ ID NO 11, SEQ ID NO 13, SEQ ID NO 15, SEQ ID NO 17, SEQ ID NO 19, SEQ ID NO 21, SEQ ID NO 23, SEQ ID NO 25, SEQ ID NO 27, SEQ ID NO 29, SEQ ID NO 31, SEQ ID NO 33, SEQ ID NO 35, SEQ ID NO 37, SEQ ID NO 39, SEQ ID NO 41, SEQ ID NO 43, SEQ ID NO 45, SEQ ID NO 47, SEQ ID NO 49, SEQ ID NO 51, SEQ ID NO 106 or (ii) a nucleotide sequence complementary to a sequence according to (I), or (iii) a nucleotide sequence showing at least 95%, preferably 96%, 97%, 98% and most preferably 99% homology to the fill length of a sequence according to (I), or (iv) a nucleotide sequence according to (I) whereby T is replaced by U, or (v) a

nucleotide sequence according to (I) whereby at least one nucleotide is substituted by a nucleotide analogue.

5. A nucleic acid fragment consisting of a sequence of at least 15, preferably 16, 17, 18, 19, 20, 21, 22, 23, 24, 25 up to 50 contiguous nucleotides of the sequence of a polynucleic acid according to claim 4, with said nucleic acid fragment being characterized by the fact that it selectively hybridizes to said polynucleic acid and/or selectively amplifies said polynucleic acid.

6. A virus strain belonging to **HIV**-1 group O, comprising in its genome a nucleic acid according to claim 4, and more particularly comprising in its genome the RNA equivalent of one of the DNA sequences represented by SEQ ID NO 1, SEQ ID NO 3, SEQ ID NO 5, SEQ ID NO 7, SEQ ID NO 9, SEQ ID NO 11, SEQ ID NO 13, SEQ ID NO 15, SEQ ID NO 17, SEQ ID NO 19, SEQ ID NO 21, SEQ ID NO 23, SEQ ID NO 25, SEQ ID NO 27, SEQ ID NO 29, SEQ ID NO 31, SEQ ID NO 33, SEQ ID NO 35, SEQ ID NO 37, SEQ ID NO 39, SEQ ID NO 106 and/or one of the DNA sequences represented by SEQ ID NO 41, SEQ ID NO 43, SEQ ID NO 45, SEQ ID NO 47, SEQ ID NO 49, SEQ ID NO 51, and/or a variant sequence of the above-mentioned DNA sequences, said variant sequence showing at least 95% homology with the entire length of one of the above-mentioned sequences.

7. A virus strain according to claim 6, deposited at the ECACC on Jun. 13, 1997 under accession number V97061301, V97061302 or V97061303, or deposited at the ECACC on Jul. 13, 1998, under provisional accession number V98071301 or V98071302.

8. A polynucleic acid isolated from an **HIV**-1 group O strain according to any of claims 6 to 7.

9. An antigen isolated from an **HIV**-1 group O strain according to any of claims 6 to 7.

10. An antibody, preferably a monoclonal antibody, raised against an antigen or antigen fragment according to any of claims 1 to 3, or claim 9, with said antibody recognizing specifically the antigen or the antigen fragment to which it has been raised.

11. A method for detecting the presence of an **HIV**-1 infection, said method comprising the detection of antibodies against **HIV**-1, including **HIV**-1 group O, using an antigen or antigen fragment according to any of claims 1 to 3, or claim 9, and/or the detection of viral antigen originating from **HIV**-1, including **HIV**-1 group O, using an antibody according to claim 10, and/or the detection of viral nucleic acid originating from **HIV**-1, including **HIV**-1 group O, using a nucleic acid or nucleic acid fragment according to claims 4 or 5, or claim 8, in a biological sample.

12. A kit for the detection of the presence of an **HIV**-1 infection, comprising at least one of the antigens or antigen fragments according to any of claims 1 to 3, or claim 9, and/or at least one of the nucleic acids or nucleic acid fragments according to claim 4 or 5, or claim 8 and/or an antibody according to claim 10.

13. A vaccine composition which provides protective immunity against an **HIV**-1 infection, including an **HIV**-1 type O infection, comprising as an active principle at least one antigen or antigen fragment according to claims 1 to 3, or 9, or at least one nucleic acid according to claims 4 to 5, or 8 or a virus like particle (VLP) comprising at least one antigen or antigen fragment according to claims 1 to 3, or 9, or an attenuated form of at least one of the **HIV**-1 type O strains according to claims 6 to 7, said active principle being combined with a pharmaceutically acceptable carrier.

L11 ANSWER 4 OF 21 USPATFULL on STN
2003:257274 Lentivirus from the group of immunodeficiency viruses of drill monkeys (Mandrillus leucophaeus) and their use.
Guertler, Lutz Gerhard, Greifswald, GERMANY, FEDERAL REPUBLIC OF
Hauser, Hans Peter, Marburg, GERMANY, FEDERAL REPUBLIC OF
Dongmo Deloko, Yvette Beatrice, Muenchen, GERMANY, FEDERAL REPUBLIC OF
Zekeng, Leopold, Yaounde, CAMEROON
Kaptue, Lazare, Yaounde, CAMEROON
US 2003180324 A1 20030925
APPLICATION: US 2003-364360 A1 20030212 (10)
PRIORITY: DE 1999-19936003 19990803
DOCUMENT TYPE: Utility; APPLICATION.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The present invention relates to an immunodeficiency virus of drill monkeys, its RNA, the corresponding cDNA, proteins derived therefrom and fragments of the nucleic acids or proteins. The invention likewise relates to the diagnostic use of the nucleic acids and proteins mentioned and their fragments and to a diagnostic.

CLM What is claimed is:

1. The immunodeficiency virus SIM27, whose RNA or a part thereof is complementary to the sequence according to Table 2 or Table 3 or Table 4 or Table 5 or Table 6 or Table 7.

2. A variant of the immunodeficiency virus as claimed in claim 1, comprising an RNA which is complementary to a DNA which is investigated by the following process: (a) extraction of the sequences mentioned in Table 11 from the gene database "Genbank" and loading of the sequences including the sequence to be investigated into the computer program "ClustalW Version 1.74", (b) multiple alignment of the sequences according to Table 11 and of the sequence to be investigated and phylogenetic analysis of the data obtained by the neighbor-joining method by means of the computer program "ClustalW Version 1.74", (c) visualization of the family tree data obtained as a family tree using a suitable presentation program, wherein the variant branches off along the distance from the end up to the first branching point from the branch of the family tree on the end of which SIM27 is located.

3. The GAG protein of SIM27 or a variant thereof, which is investigated by the following process: (a) extraction of the GAG portions of the sequences mentioned in Table 11 from the gene database "Genbank" and loading of the corresponding amino acid sequences into the computer program "ClustalW Version 1.74", (b) multiple alignment of these amino acid sequences with the sequence according to Table 8 and phylogenetic analysis of the data obtained by the neighbor-joining method by means of the computer program "ClustalW Version 1.74", (c) visualization of the family tree data obtained as a family tree using a suitable presentation program; wherein the variant branches off along the distance from the end up to the first branching point from the branch of the family tree on the end of which SIM27-gag is located.

4. The Env protein of SIM27 or a variant thereof, which is investigated by the following process: (a) extraction of the ENV portions of the sequences mentioned in Table 11 from the gene database "Genbank" and loading of the corresponding amino acid sequences into the computer program "ClustalW Version 1.74", (b) multiple alignment of these amino acid sequences with the sequences according to Table 10 and phylogenetic analysis of the data obtained by the neighbor-joining method by means of the computer program "ClustalW Version 1.74", (c) visualization of the family tree data obtained as a family tree using a suitable presentation program; wherein the variant branches off along the distance from the end up to the first branching point from the branch of the family tree on the end of which SIM27-env is located.

5. The POL protein of SIM27 or a variant thereof, which is investigated by the following process: (a) extraction of the POL portions of the sequences mentioned in Table 11 from the gene database "Genbank" and

loading of the corresponding amino acid sequences into the computer program "ClustalW Version 1.74", (b) multiple alignment of these amino acid sequences with the sequences according to Table 9 and phylogenetic analysis of the data obtained by the neighbor-joining method by means of the computer program "ClustalW Version 1.74", (c) visualization of the family tree data obtained as a family tree using a suitable presentation program; wherein the variant branches off along the distance from the end up to the first branching point from the branch of the family tree on the end of which SIM27-pol is located.

6. The use of a virus as claimed in claim 1 or of a protein as claimed in one or more of claims 3 to 5 for the detection of antibodies directed against an immunodeficiency virus in a sample.

L11 ANSWER 5 OF 21 USPATFULL on STN
2003:253523 Detection of **HIV**-1 by nucleic acid amplification.
Bee, Gary G., Vista, CA, United States
Yang, Yeasing Y., San Diego, CA, United States
Kolk, Dan, Ramona, CA, United States
Giachetti, Cristina, Solana Beach, CA, United States
McDonough, Sherrol H., San Diego, CA, United States
Gen-Probe Incorporated, San Diego, CA, United States (U.S. corporation)
US 6623920 B1 20030923
APPLICATION: US 2000-611627 20000707 (9)
PRIORITY: US 1999-143072P 19990709 (60)
DOCUMENT TYPE: Utility; GRANTED.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Nucleic acid sequences and methods for detecting **HIV**-1 nucleic acid (LTR and pol sequences) in biological samples by detecting amplified nucleic acids are disclosed. Kits comprising nucleic acid oligomers for amplifying **HIV**-1 nucleic acid present in a biological sample and detecting the amplified nucleic acid are disclosed.
CLM What is claimed is:
1. A method of detecting **HIV**-1 nucleic acid in a biological sample, comprising the steps of: providing a biological sample containing **HIV**-1 nucleic acid; contacting the biological sample with at least one capture oligomer comprising a base sequence that hybridizes specifically to a target region in LTR or pol sequences of **HIV**-1 nucleic acid, thus forming a capture oligomer:**HIV**-1 nucleic acid complex; separating the capture oligomer:**HIV**-1 nucleic acid complex from the biological sample; then amplifying the LTR or pol sequences, or a cDNA made therefrom, using a nucleic acid polymerase in vitro to produce an amplified product; and detecting the amplified product using a labeled detection probe that hybridizes specifically with the amplified product, thereby indicating presence of the **HIV**-1 nucleic acid in the biological sample.

2. The method of claim 1, wherein the contacting step uses a capture oligomer further comprising a tail sequence that binds to a complementary sequence immobilized on a solid support.

3. The method of claim 1, wherein the base sequence of the capture oligomer that hybridizes specifically to a target region in the LTR sequence is a sequence of about 22 to about 54 bases including about 22 bases consisting essentially of LTR-specific bases contained in SEQ ID NO:2.

4. The method of claim 1, wherein the capture oligomer comprises an LTR-specific oligomer of about 22 to about 55 bases including about 22 bases consisting essentially of LTR-specific bases contained in SEQ ID NO:2 and optionally one or more oligomers that hybridize specifically to a target region in the pol sequence.

5. The method of claim 4, wherein the capture oligomer is a combination of at least two oligomers wherein one oligomer is an LTR-specific

oligomer of about 22 to about 55 bases including about 22 bases consisting essentially of LTR-specific bases contained in SEQ ID NO:2 and at least one oligomer that hybridizes specifically to a pol sequence.

6. The method of claim 1, wherein the amplifying step uses at least two amplification oligomers that bind specifically to LTR or pol sequences or sequences complementary to LTR or pol sequences.

7. The method of claim 6, wherein the amplifying step uses amplification oligomers for amplifying LTR sequences consisting essentially of SEQ ID NO:7 and SEQ ID NO:9.

8. The method of claim 6, wherein the amplifying step uses at least two amplification oligomers for amplifying pol sequences consisting essentially of sequences of: SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12 or SEQ ID NO:14.

9. The method of claim 1, wherein the amplifying step comprises a transcription-associated amplification method that uses: at least one promoter-primer comprising a promoter sequence that is recognized by an RNA polymerase when the promoter sequence is double stranded, wherein the promoter sequence is covalently attached to the 5' end of a LTR-specific sequence consisting essentially of SEQ ID NO:7, or a pol-specific sequence consisting essentially of SEQ ID NO:12 or SEQ ID NO:14; and at least one primer selected from a LTR-specific sequence consisting essentially of SEQ ID NO:9, or a pol-specific sequence consisting essentially of SEQ ID NO:10 or SEQ ID NO:11, provided that the LTR-specific promoter-primer is combined with the LTR-specific primer for amplifying a LTR target region, and/or at least one pol-specific promoter-primer is combined with at least one pol-specific primer for amplifying a pol target region.

10. The method of claim 9, wherein the amplifying step uses any of the following combinations of promoter-primers and primers: promoter-primers consisting essentially of SEQ ID NO:12 and SEQ ID NO:14, with primers consisting essentially of SEQ ID NO:10 and SEQ ID NO:11; promoter-primers consisting essentially of SEQ ID NO:7, SEQ ID NO:12 and SEQ ID NO:14, with primers consisting essentially of SEQ ID NO:9, SEQ ID NO:10 and SEQ ID NO:11; a promoter-primer consisting essentially of SEQ ID NO:12, and a primer consisting essentially of SEQ ID NO:10; or a promoter-primer consisting essentially of SEQ ID NO:7, and a primer consisting essentially of SEQ ID NO:9.

11. The method of claim 1, wherein the detecting step uses at least one labeled detection probe having a base sequence selected from: a LTR-specific sequence consisting essentially of SEQ ID NO:16, a pol-specific sequence consisting essentially of SEQ ID NO:17, or a pol-specific sequence consisting essentially of SEQ ID NO:18.

12. The method of claim 1, wherein the detecting step uses a combination of at least two labeled detection probes, wherein the probe base sequences are about 20 bases consisting essentially of SEQ ID NO:16, about 22 to about 30 bases consisting essentially of SEQ ID NO:17, or about 17 to about 20 bases consisting essentially of SEQ ID NO:18.

13. The method of claim 12, wherein the labeled detection probe consisting essentially of SEQ ID NO:16 has an inosine at position 7.

14. The method of claim 1, wherein the detecting step uses a labeled detection probe of about 20 bases consisting essentially of SEQ ID NO:16.

15. The method of claim 1, wherein the detecting step uses at least one labeled detection probe of about 22 to about 30 bases consisting essentially of SEQ ID NO:17, or about 17 to about 20 bases consisting

essentially of SEQ ID NO:18.

16. The method of claim 1, wherein the detecting step uses at least one labeled detection probe that includes at least one 2'-methoxy backbone linkage.

17. The method of claim 1, wherein: the contacting step uses capture oligomers made up of LTR-specific bases consisting essentially of about 22 LTR-specific bases contained in SEQ ID NO:2 and a tail sequence of about 5 to 50 bases that are not LTR-specific and provide a means of capturing **HIV**-1 nucleic acid hybridized to the LTR-specific sequence from the other components in the biological sample; the amplifying step uses promoter-primers consisting essentially of the sequences of SEQ ID NO:7, SEQ ID NO:12 and SEQ ID NO:14 and primers consisting essentially of the sequences of SEQ ID NO:9, SEQ ID NO:10 and SEQ ID NO:11; and the detecting step uses labeled detection probes wherein probe base sequences are about 20 bases consisting essentially of SEQ ID NO:16, about 22 to about 30 bases consisting essentially of SEQ ID NO:17 and about 17 to about 20 bases consisting essentially of SEQ ID NO:18.

18. The method of claim 1, wherein: the contacting step uses at least two capture oligomers that hybridize to different sequences in the target region; the amplifying step uses at least two different promoter-primers that hybridize to a first set of sequences within the target region and at least two different primers that hybridize to a second set of sequences within the target region; and the detecting step uses at least two labeled probes that bind specifically to different sequences located between the first set and second set of sequences within the target region.

19. The method of claim 18, wherein: the contacting step uses capture oligomers having sequences that hybridize specifically to pol sequences; the amplifying step uses promoter-primers consisting essentially of sequences of SEQ ID NO:12 and SEQ ID NO:14 and primers consisting essentially of the sequences of SEQ ID NO:10 and SEQ ID NO:11; and the detecting step uses labeled probes of about 22 to about 30 bases consisting essentially of SEQ ID NO:17 and about 17 to about 20 bases consisting essentially of SEQ ID NO:18.

20. The method of claim 18, wherein the amplifying step uses at least two promoter-primers that hybridize to a first set of overlapping sequences within the target region, at least two primers that hybridize to a second set of overlapping sequences within the target region, or at least two promoter-primers that hybridize to a first set of overlapping sequences within the target region and at least two primers that hybridize to a second set of overlapping sequences within the target region.

21. A kit comprising a combination of oligomers, wherein the oligomers contained in the kit have sequences consisting essentially of SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:17 and SEQ ID NO:18, and wherein the oligomers consisting essentially of the sequences of SEQ ID NO:17 and SEQ ID NO:18 are labeled with a detectable label.

22. The kit of claim 21, also containing oligomers with base sequences consisting essentially of the sequences of SEQ ID NO:7, SEQ ID NO:9 and SEQ ID NO:16, wherein the oligomer consisting essentially of SEQ ID NO:16 is labeled with a detectable label.

23. The method of claim 21, wherein the oligomer consisting essentially of SEQ ID NO:16 has an inosine at position 7.

24. A composition comprising a combination of at least two oligomers selected from the group consisting of: SEQ ID NO:7, optionally with a promoter sequence covalently attached to the 5' end of SEQ ID NO:7; and SEQ ID NO;9.

25. The composition of claim 24, wherein the promoter sequence is a T7 RNA polymerase promoter sequence.

26. The composition of claim 24, wherein SEQ ID NO:7 with the promoter sequence covalently attached to the 5' end is SEQ ID NO:8.

27. The composition of claim 24, wherein the composition further comprises an oligomer of SEQ ID NO:16 containing an inosine base.

28. The composition of claim 27, wherein an oligomer base sequence is linked by a backbone that includes at least one 2'-methoxy RNA group, at least one 2' fluoro-substituted RNA group, at least one peptide nucleic acid linkage, at least one phosphorohioate linkage, at least one methylphosphonate linkage or any combination thereof.

29. The composition of claim 27, wherein the oligomer of SEQ ID NO:16 containing an inosine base comprises at least one 2'-methoxy RNA group in the backbone.

30. The composition of claim 27, wherein the oligomer of SEQ ID NO:16 containing an inosine base comprises a detectable label joined directly or indirectly to the oligomer.

31. The composition of claim 30, wherein the detectable label is a chemiluminescent compound.

32. An oligomer consisting of SEQ ID NO:1, wherein the oligomer includes at least one 2'-methoxy RNA group, and wherein SEQ ID NO:1 may be optionally covalently joined with a 3' homopolymeric tail of about 30 bases.

33. A composition comprising a combination of at least two oligomers selected from the group consisting of: SEQ ID NO:12, optionally with a promoter sequence covalently attached to the 5' end of SEQ ID NO:12; SEQ ID NO:14, optionally with a promoter sequence covalently attached to the 5' end of SEQ ID NO:14; SEQ ID NO:10; and SEQ ID NO: 11.

34. The composition of claim 33, wherein the combination further comprises at least one oligomer selected from the group consisting of: SEQ ID NO:17, and SEQ ID NO:18 containing an inosine base.

35. The composition of claim 34, wherein an oligomer base sequence is linked by a backbone that includes at least one 2'-methoxy RNA group, at least one 2' fluro-substituted RNA group, at least one peptide nucleic acid linkage, at least one phosphorothioate linkage, at least one methylphosphonate linkage or any combination thereof.

36. The composition of claim 34, wherein the oligomer of SEQ ID NO:17 or SEQ ID NO:18 containing an Inosine base comprises at least one 2'-methoxy RNA group in the backbone.

37. The composition of claim 34, wherein the oligomer of SEQ ID NO:17 or SEQ ID NO:18 containing an inosine base comprises a detectable label joined directly or indirectly to the oligomer.

38. The composition of claim 37, wherein the detectable label is a chemiluminescent compound.

L11 ANSWER 6 OF 21 USPATFULL on STN
2003:251164 RNA interference mediated inhibition of **HIV** gene expression using short interfering RNA.
McSwiggen, James A., Boulder, CO, UNITED STATES
US 2003175950 A1 20030918
APPLICATION: US 2002-225023 A1 20020821 (10)

PRIORITY: US 2002-398036P 20020723 (60)
US 2001-294140P 20010529 (60)
DOCUMENT TYPE: Utility; APPLICATION.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention concerns methods and reagents useful in modulating **HIV** gene expression in a variety of applications, including use in therapeutic, diagnostic, target validation, and genomic discovery applications. Specifically, the invention relates to small interfering RNA (siRNA) molecules capable of mediating RNA interference (RNAi) against **HIV** polypeptide and polynucleotide targets.
CLM What is claimed is:
1. A short interfering RNA (siRNA) molecule that down regulates expression of a **human immunodeficiency virus** (**HIV**) gene by RNA interference.

2. The siRNA molecule of claim 1, wherein said siRNA molecule is adapted for use to treat **HIV** infection or acquired immunodeficiency syndrome (AIDS).

3. The siRNA molecule of claim 1, wherein said siRNA molecule comprises a sense region and an antisense region and wherein said antisense region comprises sequence complementary to a **HIV** RNA sequence and the sense region comprises sequence complementary to the antisense region.

4. The siRNA molecule of claim 3, wherein said siRNA molecule is assembled from two nucleic acid fragments wherein one fragment comprises the sense region and the second fragment comprises the antisense region of said siRNA molecule.

5. The siRNA molecule of claim 4, wherein said sense region and antisense region are covalently connected via a linker molecule.

6. The siRNA molecule of claim 5, wherein said linker molecule is a polynucleotide linker.

7. The siRNA molecule of claim 5, wherein said linker molecule is a non-nucleotide linker.

8. The siRNA molecule of claim 3, wherein said antisense region comprises sequence complementary to sequence having any of SEQ ID NOs. 1-738.

9. The siRNA molecule of claim 3, wherein said antisense region comprises sequence having any of SEQ ID NOs. 739-1476.

10. The siRNA molecule of claim 3, wherein said sense region comprises sequence having any of SEQ ID NOs. 1-738.

11. The siRNA molecule of claim 3, wherein said sense region comprises a 3'-terminal overhang and said antisense region comprises a 3'-terminal overhang.

12. The siRNA molecule of claim 11, wherein said 3'-terminal overhangs each comprise about 2 nucleotides.

13. The siRNA molecule of claim 11, wherein said antisense region 3'-terminal nucleotide overhang is complementary to a **HIV** RNA.

14. The siRNA molecule of claim 3, wherein said sense region comprises one or more 2'-O-methyl modified pyrimidine nucleotides.

15. The siRNA molecule of claim 3, wherein said sense region comprises a terminal cap moiety at the 5'-end, 3'-end, or both 5' and 3' ends of said sense region.

16. The siRNA molecule of claim 3, wherein said antisense region

comprises one or more 2'-deoxy-2'-fluoro modified pyrimidine nucleotides.

17. The siRNA molecule of claim 3, wherein said antisense region comprises a phosphorothioate internucleotide linkage at the 3' end of said antisense region.

18. The siRNA molecule of claim 3, wherein said antisense region comprises between about one and about five phosphorothioate internucleotide linkages at the 5' end of said antisense region.

19. The siRNA molecule of claim 11, wherein said 3'-terminal nucleotide overhangs comprise ribonucleotides that are chemically modified at a nucleic acid sugar, base, or backbone.

20. The siRNA molecule of claim 11, wherein said 3'-terminal nucleotide overhangs comprise deoxyribonucleotides that are chemically modified at a nucleic acid sugar, base, or backbone.

21. The siRNA molecule of claim 11, wherein said 3'-terminal nucleotide overhangs comprise one or more universal base ribonucleotides.

22. The siRNA molecule of claim 11, wherein said 3'-terminal nucleotide overhangs comprise one or more acyclic nucleotides.

23. The siRNA molecule of claim 11, wherein said 3'-terminal nucleotide overhangs comprise nucleotides comprising internucleotide linkages having Formula I: ##STR7## wherein each R1 and R2 is independently any nucleotide, non-nucleotide, or polynucleotide which can be naturally occurring or chemically modified, each X and Y is independently O, S, N, alkyl, or substituted alkyl, each Z and W is independently O, S, N, alkyl, substituted alkyl, O-alkyl, S-alkyl, alkaryl, or aralkyl, and wherein W, X, Y and Z are not all O.

24. The siRNA molecule of claim 11, wherein said 3'-terminal nucleotide overhangs comprise nucleotides or non-nucleotides having Formula II: ##STR8## wherein each R3, R4, R5, R6, R7, R8, R10, R11 and R12 is independently H, OH, alkyl, substituted alkyl, alkaryl or aralkyl, F, Cl, Br, CN, CF3, OCF3, OCN, O-alkyl, S-alkyl, N-alkyl, O-alkenyl, S-alkenyl, N-alkenyl, SO-alkyl, alkyl-OSH, alkyl-OH, O-alkyl-OH, O-alkyl-SH, S-alkyl-OH, S-alkyl-SH, alkyl-S-alkyl, alkyl-O-alkyl, ONO2, NO2, N3, NH2, aminoalkyl, aminoacid, aminoacyl, ONH2, O-aminoalkyl, O-aminoacid, O-aminoacyl, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalklylamino, substituted silyl, or group having Formula I; R9 is O, S, CH2, S.dbd.O, CHF, or CF2, and B is a nucleosidic base or any other non-naturally occurring base that can be complementary or non-complementary to **HIV** RNA or a non-nucleosidic base or any other non-naturally occurring universal base that can be complementary or non-complementary to **HIV** RNA.

25. An expression vector comprising a nucleic acid sequence encoding at least one siRNA molecule of claim 1 in a manner that allows expression of the nucleic acid molecule.

26. A mammalian cell comprising an expression vector of claim 25.

27. The mammalian cell of claim 26, wherein said mammalian cell is a human cell.

28. The expression vector of claim 25, wherein said siRNA molecule comprises a sense region and an antisense region and wherein said antisense region comprises sequence complementary to a **HIV** RNA sequence and the sense region comprises sequence complementary to the antisense region.

29. The expression vector of claim 28, wherein said siRNA molecule

comprises two distinct strands having complementarity sense and antisense regions.

30. The expression vector of claim 28, wherein said siRNA molecule comprises a single strand having complementary sense and antisense regions.

L11 ANSWER 7 OF 21 USPATFULL on STN
2003:231970 Complete genome sequence of a simian immunodeficiency virus from a red-capped mangabey.
Hahn, Beatrice H., Birmingham, AL, UNITED STATES
Gao, Feng, Hoover, AL, UNITED STATES
Shaw, George M., Birmingham, AL, UNITED STATES
Marx, Preston A., Covington, LA, UNITED STATES
Smith, Stephen M., Essex Fells, NJ, UNITED STATES
Georges-Courbot, Marie Claude, Paris XV, FRANCE
Lu, Chang Yong, Forest Hills, NY, UNITED STATES
UAB Research Foundation (U.S. corporation)
US 2003162170 A1 20030828
APPLICATION: US 2003-369294 A1 20030218 (10)
DOCUMENT TYPE: Utility; APPLICATION.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The nucleotide sequence and deduced amino acid sequences of the complete genome of a simian immunodeficiency virus isolate from a red-capped mangabey are disclosed. The invention relates to the nucleic acids and peptides encoded by and/or derived from these sequences and their use in diagnostic methods and as immunogens.
CLM What is claimed is:
1. A nucleic acid comprising the nucleotide sequence of the genome of the simian immunodeficiency virus isolate SIVrcm shown in SEQ ID NO:1 or a complementary sequence thereof.

2. The nucleic acid of claim 1, wherein said nucleic acid comprises a nucleotide sequence of at least 12 contiguous bases of said nucleic acid or a complementary sequence thereof.

3. The nucleic acid of claim 1, wherein said nucleic acid comprises a nucleotide sequence of a LTR of said nucleic acid or a complementary sequence thereof.

4. The nucleic acid of claim 1, wherein said nucleic acid encodes a polypeptide selected from the group consisting of Gag, Pol, Vif, Vpr, Env, Tat, Rev, Nef and Vpx of SIVrcm.

5. The nucleic acid of claim 1, wherein said nucleic acid has a nucleotide sequence which is derived from SEQ ID NO:1.

6. A vector comprising the nucleic acid of claim 1.

7. A cell comprising the nucleic acid of claim 1.

8. A cell comprising the vector of claim 6.

9. A composition comprising the nucleic acid of claim 1 and a physiologically acceptable carrier.

10. A method for producing a polypeptide encoded by the nucleic acid of claim 1, comprising the step of growing a cell comprising the nucleic acid of claim 1 under conditions such that the encoded polypeptide is produced.

11. The method of claim 10, wherein said polypeptide comprises a contiguous sequence of at least 13 amino acids.

12. A composition comprising the polypeptide produced by the method of

claim 10 and a physiologically acceptable carrier.

13. A method for producing a polypeptide encoded by the nucleic acid of claim 1, comprising the step of growing a cell comprising a vector, said vector comprising the nucleic acid of claim 1, under conditions such that the encoded polypeptide is produced.

14. The method of claim 13, wherein said polypeptide comprises a contiguous sequence of at least 13 amino acids.

15. A composition comprising the polypeptide produced by the method of claim 13 and a physiologically acceptable carrier.

16. A method of inducing serum antibodies that bind at least one polypeptide encoded by the nucleic acid of claim 1, said method comprising: administering to a mammal, in a physiologically acceptable carrier, an amount of said encoded polypeptide sufficient to elicit production of said antibodies.

17. An anti-SIVrcm antibody made by the method of claim 16.

18. A composition comprising an antibody according to claim 17 and a physiologically acceptable carrier.

19. A method for detecting the presence of SIVrcm in a sample comprising contacting said sample with the antibody of claim 17 under conditions that allow the formation of an antibody-antigen complex and detecting said complex.

20. A kit for detecting the presence of SIVrcm in a sample comprising an antibody of claim 17.

21. A method of inducing serum antibodies that bind at least one polypeptide encoded by the nucleic acid of claim 1, said method comprising: administering to a mammal, in a physiologically acceptable carrier, the nucleic acid of claim 1 encoding said polypeptide and which produces an immunologically sufficient amount of the encoded polypeptide to elicit said antibodies.

22. An antibody to SIVrcm made by the method of claim 21.

23. A composition comprising an antibody according to claim 22, and a physiologically acceptable carrier.

24. A method for detecting the presence of SIVrcm in a sample comprising contacting said sample with the antibody of claim 22 under conditions that allow the formation of an antibody-antigen complex and detecting said complex.

25. A kit for detecting the presence of SIVrcm in a sample comprising an antibody of claim 22.

26. A method for detecting the presence of antibodies to SIVrcm in a sample comprising contacting said sample with a polypeptide encoded by the nucleic acid of claim 1 under conditions that allow the formation of an antibody-antigen complex and detecting the complex.

27. A method for detecting the presence of SIVrcm in a sample comprising contacting said sample with the nucleic acid of claim 1 and detecting said nucleic acid bound to the genomic DNA, mRNA or cDNA of the SIVrcm virus.

28. A kit for detecting the presence of SIVrcm in a sample comprising the nucleic acid of claim 1.

29. A nucleic acid probe comprising a sequence of at least 19 contiguous

nucleotides derived from the nucleic acid of claim 1, or the complementary sequence thereof.

30. A composition comprising a nucleic acid according to claim 29.

31. A method of detecting the presence of SIVrcm in a biological sample comprising: a.) contacting the nucleic acid of the biological sample with the nucleic acid probe of claim 29; and b.) detecting the presence or absence of complexes formed between said nucleic acid of the biological sample and said nucleic acid probe.

32. A method of detecting the presence of SIVrcm in a biological sample comprising: a). contacting said biological sample with at least two nucleic acid probes of claim 29; b). amplifying the RNA of the biological sample via reverse transcription-polymerase chain reaction to produce amplification products; and c.) detecting the presence or absence of amplification products.

33. A method for analyzing a first nucleotide sequence comprising comparing the nucleotide sequence of claim 1 with said first sequence.

L11 ANSWER 8 OF 21 USPATFULL on STN
2003:225848 Non-M, non-O **HIV**-1 strains, fragments and uses.
Mauclere, Phillippe, Bordeaux, FRANCE
Loussert-Ajaka, Ibtissam, Sartrouville, FRANCE
Simon, Francois, Paris, FRANCE
Saragosti, Sentob, Billancourt, FRANCE
Barre-Sinoussi, Francoise, Moulimeaux, FRANCE
Institute National de la Sante et de La Recherche Medicale-Inserm (non-U.S. corporation)
US 2003157660 A1 20030821
APPLICATION: US 2002-301661 A1 20021122 (10)
PRIORITY: FR 1996-15087 19961209
DOCUMENT TYPE: Utility; APPLICATION.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Retroviral strains of the non-M, non-O **HIV**-1 group, in particular a strain designated YBF30, its fragments and also its uses as a diagnostic reagent and as an immunogenic agent.

The **HIV**-1 viruses which differ both from the M group and the O group exhibit the following characteristics:

little or no serological reactivity with regard to the proteins of the M and O groups and strong serological reactivity with regard to the proteins which are derived from the strain YBF30 according to the invention or the strain CPZGAB SIV;

absence of genomic amplification when using primers from the env and gag regions of the M and O **HIV**-1 groups;

genomic amplification in the presence of primers which are derived from the YBF30 strain according to the invention; and

homology of the products of the envelope gene which is greater than 70% with regard to the YBF30 strain.

CLM What is claimed is:
1) Non-M, non-O **HIV**-1 strain which exhibits the morphological and immunological characteristics of the retrovirus which was deposited on Jul. 2, 1996 under number I-1753 (designated YBF30) in the Collection Nationale de Cultures de Microorganismes (National Collection of Microorganism Cultures) kept by the Pasteur Institute.

2) Nucleic acid sequences, characterized in that they are derived from the strain according to claim 1.

3) Nucleic acid sequence according to claim 2, characterized in that it is selected from the group consisting of the following sequences: the complete nucleotide sequence of the strain according to claim 1 (SEQ ID No.1) as well as nucleic acid fragments which are derived from the said strain: (SEQ ID No.2), (SEQ ID No.3), (SEQ ID No.5), (SEQ ID No.7), (SEQ ID No.9), (SEQ ID No.11), (SEQ ID No.13), (SEQ ID No.15), (SEQ ID No.17), (SEQ ID No.19) and the sequences SEQ ID No. 21-57, and also any sequence which is not identical to one of the above nucleotide sequences, or is not complementary to one of these sequences, but is nevertheless capable of hybridizing with a nucleic acid sequence which is derived from a non-M, non-O **HIV**-1 virus.

4) Oligonucleotide, characterized in that it is selected from the sequences SEQ ID No. 21 to 57, and in that it is capable of being used as a primer or as a probe for detecting an **HIV**-1 according to claim 1 or claim 5.

5) **HIV**-1 viruses, characterized in that they differ both from the M group and from the O group and exhibit the following characteristics: little or no serological reactivity with regard to proteins of the M and O groups and strong serological reactivity with regard to proteins which are derived from the YBF30 strain according to claim 1 or the CPZGAB SIV strain; absence of genomic amplification when using primers from the env and gag regions of the **HIV**-1 viruses of the M and O groups; genomic amplification in the presence of the primers which are derived from the YBF30 strain according to claim 4; and homology of the products of the envelope gene which is greater than 70% with regard to the YBF30 strain.

6) Method for diagnosing in vitro an **HIV**-1 virus of the non-M, non-O group by means of hybridization and/or gene amplification, which method is carried out using a biological sample (serum or circulating lymphocyte) and is characterized in that it comprises: a step of extracting the nucleic acid which is to be detected and which belongs to the genome of the virus, which virus may possibly be present in the biological sample, and, where appropriate, a step of treating the nucleic acid using a reverse transcriptase, if this nucleic acid is in RNA form, at least one cycle comprising the steps of denaturing the nucleic acid, of hybridizing with at least one sequence according to claim 3 or claim 4 and, where appropriate, extending the hybrid, which has been formed, in the presence of suitable reagents (polymerizing agent, such as DNA polymerase and dNTP), and a step of detecting the possible presence of the nucleic acid belonging to the genome of a virus of the non-M, non-O **HIV**-1 group type.

7) Peptide, characterized in that it can be expressed by a non-M, non-O **HIV**-1 strain according to claim 1 or claim 5 or using a nucleotide sequence according to claim 3, and in that it is capable (1) of being recognized by antibodies which are induced by a non-M, non-O **HIV**-1 virus according to claim 1 or claim 5, or a variant of this virus, and which are present in a biological sample which is obtained following an infection with a non-M, non-O **HIV**-1 strain, and/or (2) of inducing the production of anti-non-M, non-O **HIV**-1 antibodies.

8) Peptide according to claim 7, characterized in that it is selected from that which is expressed by the gag gene (SEQ ID No. 4), that which is expressed by the pol gene (SEQ ID No. 6), that which is expressed by the vif gene (SEQ ID No. 8), that which is expressed by the vpr gene (SEQ ID No. 10), that which is expressed by the vpu gene (SEQ ID No. 12), that which is expressed by the tat gene (SEQ ID No. 14), that which is expressed by the rev gene (SEQ ID No. 16), that which is expressed by the env gene (SEQ ID No. 18) or one of its fragments such as a fragment of the V3 loop region (SEQ ID No. 58), and that which is expressed by the nef gene (SEQ ID No. 20), or a fragment of these peptides which are capable of recognizing the antibodies which are produced during an infection with an **HIV**-1 virus according to claim 1 or claim 5.

9) Immunogenic compositions which comprise one or more translation products of the nucleotide sequences according to claim 3 and/or one of the peptides according to claim 7 or claim 8.

10) Antibodies which are directed against one or more of the peptides according to claim 7 or claim 8.

11) Method for the in-vitro diagnosis of a non-M, non-O **HIV**-1 virus, characterized in that it comprises bringing into contact a biological sample, which has been withdrawn from a patient, with antibodies according to claim 10, which may possibly be combined with anti-CPZGAB SIV antibodies, and detecting the immunological complexes which are formed between the **HIV**-1 antigens, which may possibly be present in the biological sample, and the said antibodies.

L11 ANSWER 9 OF 21 USPATFULL on STN
2003:180685 Enzymatic nucleic acid treatment of diseases or conditions related to levels of **HIV**.
McSwiggen, James, Boulder, CO, UNITED STATES
US 2003124513 A1 20030703
APPLICATION: US 2002-157580 A1 20020529 (10)
PRIORITY: US 2001-294140P 20010529 (60)
DOCUMENT TYPE: Utility; APPLICATION.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The present invention relates to nucleic acid molecules, including enzymatic nucleic acid molecules, such as hammerhead ribozymes, DNAzymes, siRNA, aptamers, decoys and allozymes, which modulate the expression of **HIV** genes.

CLM What is claimed is:

1. A siRNA nucleic acid molecule which modulates expression of a nucleic acid molecule encoding **HIV** or a component of **HIV**.

2. An enzymatic nucleic acid molecule which modulates expression of a nucleic acid molecule encoding **HIV** or a component of **HIV**, wherein said enzymatic nucleic acid molecule is in an Inozyme, G-cleaver, Zinzyme or Amberzyme configuration.

3. An enzymatic nucleic acid molecule comprising a sequence selected from the group consisting of SEQ ID NOs. 77-139 and 149-158.

4. An enzymatic nucleic acid molecule comprising at least one binding arm wherein one or more of said binding arms comprises a sequence complementary to a sequence selected from the group consisting of SEQ ID NOs. 1-76 and 140-148.

5. A siRNA nucleic acid molecule comprising a sequence complementary to a sequence selected from the group consisting of SEQ ID NOs. 1-76 and 140-148.

6. The nucleic acid of any of claims 1-5, wherein said nucleic acid molecule is adapted to **HIV** infection or acquired immunodeficiency syndrome (AIDS).

7. The enzymatic nucleic acid molecule of any of claims 2-4, wherein said enzymatic nucleic acid molecule has an endonuclease activity to cleave RNA having a **HIV** sequence.

8. The enzymatic nucleic acid molecule of claim 2, wherein said enzymatic nucleic acid molecule is in an Inozyme configuration.

9. The enzymatic nucleic acid molecule of claim 2, wherein said enzymatic nucleic acid molecule is in a Zinzyme configuration.

10. The enzymatic nucleic acid molecule of claim 2, wherein said

enzymatic nucleic acid molecule is in a G-cleaver configuration.

11. The enzymatic nucleic acid molecule of claim 2, wherein said enzymatic nucleic acid molecule is in an Amberzyme configuration.

12. The enzymatic nucleic acid molecule of claim 4, wherein said enzymatic nucleic acid molecule is in a DNAzyme configuration.

13. The enzymatic nucleic acid molecule of claim 4, wherein said enzymatic nucleic acid molecule is in a Hammerhead configuration.

14. The enzymatic nucleic acid molecule of claim 8, wherein said Inozyme comprises a sequence complementary to a sequence selected from the group consisting of SEQ ID NOs. 7-14.

15. The enzymatic nucleic acid molecule of claim 8, wherein said Inozyme comprises a sequence selected from the group consisting of SEQ ID NOs. 83-90.

16. The enzymatic nucleic acid molecule of claim 9, wherein said Zinzyme comprises a sequence complementary to a sequence selected from the group consisting of SEQ ID NOs. 15-22 and 145-148.

17. The enzymatic nucleic acid molecule of claim 9, wherein said Zinzyme comprises a sequence selected from the group consisting of SEQ ID NOs. 91-98 and 154-158.

18. The enzymatic nucleic acid molecule of claim 11, wherein said Amberzyme comprises a sequence complementary to a sequence selected from the group consisting of SEQ ID NOs. 15-47.

19. The enzymatic nucleic acid molecule of claim 11, wherein said Amberzyme comprises a sequence selected from the group consisting of SEQ ID NOs. 112-139.

20. The enzymatic nucleic acid molecule of claim 12, wherein said DNAzyme comprises a sequence complementary to a sequence selected from the group consisting of SEQ ID NOs. 15-27 and 140-144.

21. The enzymatic nucleic acid molecule of claim 12, wherein said DNAzyme comprises a sequence selected from the group consisting of SEQ ID NOs. 99-111 and 149-153.

22. The enzymatic nucleic acid molecule of claim 13, wherein said Hammerhead comprises a sequence complementary to a sequence selected from the group consisting of SEQ ID NOs. 1-6.

23. The enzymatic nucleic acid molecule of claim 13, wherein said Hammerhead comprises a sequence selected from the group consisting of SEQ ID NOs 77-82.

24. The nucleic acid molecule of any of claims 1-5, wherein said nucleic acid molecule comprises between 12 and 100 bases complementary to a nucleic acid molecule encoding **HIV**.

25. The nucleic acid molecule of any of claims 1-5, wherein said nucleic acid molecule comprises between 14 and 24 bases complementary to a nucleic acid molecule encoding **HIV**.

26. The nucleic acid molecule of any of claims 1-5, wherein said nucleic acid molecule is chemically synthesized.

27. The nucleic acid molecule of any of claims 1-5, wherein said nucleic acid molecule comprises at least one 2'-sugar modification.

28. The nucleic acid molecule of any of claims 1-5, wherein said nucleic

acid molecule comprises at least one nucleic acid base modification.

29. The nucleic acid molecule of any of claims 1-5, wherein said nucleic acid molecule comprises at least one phosphate backbone modification.

30. A mammalian cell comprising the nucleic acid molecule of any of claims 1-5.

31. The mammalian cell of claim 30, wherein said mammalian cell is a human cell.

32. A method of reducing **HIV** activity in a cell, comprising contacting said cell with the nucleic acid molecule of any of claims 1-5, under conditions suitable for said reduction of **HIV** activity.

33. A method of treatment of a subject having a condition associated with the level of **HIV**, comprising contacting cells of said subject with the nucleic acid molecule of any of claims 1-5, under conditions suitable for said treatment.

34. The method of claim 32 further comprising the use of one or more drug therapies under conditions suitable for said treatment.

35. The method of claim 33 further comprising the use of one or more drug therapies under conditions suitable for said treatment.

36. A method of cleaving RNA of an **HIV** gene comprising contacting an enzymatic nucleic acid molecule of any of claims 2-4 with said RNA of **HIV** gene under conditions suitable for the cleavage.

37. The method of claim 36, wherein said cleavage is carried out in the presence of a divalent cation.

38. The method of claim 37, wherein said divalent cation is Mg^{2+}.

39. The nucleic acid molecule of any of claims 1-5, wherein said nucleic acid molecule comprises a cap structure, wherein the cap structure is at the 5'-end, 3'-end, or both the 5'-end and the 3'-end of said nucleic acid molecule.

40. The nucleic acid molecule of claim 39, wherein the cap structure at the 5'-end, 3'-end, or both the 5'-end and the 3'-end comprises a 3',3'-linked or 5',5'-linked deoxyabasic ribose derivative.

41. An expression vector comprising a nucleic acid sequence encoding at least one nucleic acid molecule of any of claims 1-5 in a manner which allows expression of the nucleic acid molecule.

42. A mammalian cell including an expression vector of claim 41.

43. The mammalian cell of claim 42, wherein said mammalian cell is a human cell.

44. An expression vector comprising a nucleic acid sequence encoding at least one nucleic acid molecule of any of claims 3 or 4 in a manner which allows expression of the nucleic acid molecule, wherein said nucleic acid molecule is in a hammerhead configuration.

45. The expression vector of claim 41, wherein said expression vector further comprises a sequence for a nucleic acid molecule complementary to the RNA of **HIV**.

46. The expression vector of claim 41, wherein said expression vector comprises a nucleic acid sequence encoding two or more of said nucleic acid molecules, which may be the same or different.

47. The expression vector of claim 46, wherein said expression vector further comprises a sequence encoding a siRNA nucleic acid molecule complementary to the RNA of **HIV** gene.

48. A method for treatment of acquired immunodeficiency syndrome (AIDS) or an AIDS related condition comprising administering to a subject the nucleic acid molecule of any of claims 1-5 under conditions suitable for said treatment.

49. The method of claim 48, wherein said AIDS related condition is Kaposi's sarcoma, lymphoma, cervical cancer, squamous cell carcinoma, cardiac myopathy, rheumatic disease, or opportunistic infection.

50. The method of claim 48, wherein said method further comprises administering to said subject one or more other therapies.

51. The nucleic acid molecule of claim 2 or claim 4, wherein said nucleic acid molecule comprises at least five ribose residues, at least ten 2'-O-methyl modifications, and a 3'-end modification.

52. The nucleic acid molecule of claim 51, wherein said nucleic acid molecule further comprises phosphorothioate linkages on at least three of the 5' terminal nucleotides.

53. The nucleic acid molecule of claim 51, wherein said 3'-end modification is a 3'-3' inverted abasic moiety.

54. The method of claim 34 wherein said other drug therapies are antiviral therapy, monoclonal antibody therapy, chemotherapy, radiation therapy, analgesic therapy, or anti-inflammatory therapy.

55. The method of claim 54, wherein said antiviral therapy is treatment with AZT, ddC, ddI, d4T, 3TC, Ribavirin, delvaridine, nevirapine, efravirenz, ritonavir, saquinivir, indinavir, amprenivir, nelfinavir, or lopinavir.

56. The method of claim 35 wherein said other drug therapies are antiviral therapy, monoclonal antibody therapy, chemotherapy, radiation therapy, analgesic therapy, or anti-inflammatory therapy.

57. The method of claim 56, wherein said antiviral therapy is treatment with AZT, ddC, ddI, d4T, 3TC, Ribavirin, delvaridine, nevirapine, efravirenz, ritonavir, saquinivir, indinavir, amprenivir, nelfinavir, or lopinavir.

58. The method of claim 50 wherein said other drug therapies are antiviral therapy, monoclonal antibody therapy, chemotherapy, radiation therapy, analgesic therapy, or anti-inflammatory therapy.

59. The method of claim 58, wherein said antiviral therapy is treatment with AZT, ddC, ddI, d4T, 3TC, Ribavirin, delvaridine, nevirapine, efravirenz, ritonavir, saquinivir, indinavir, amprenivir, nelfinavir, or lopinavir.

60. A composition comprising a nucleic acid molecule of any of claims 1-5 in a pharmaceutically acceptable carrier.

61. The nucleic acid molecule of claim 1 or 2, wherein said component of **HIV** is nef.

62. The nucleic acid molecule of claim 1 or 2, wherein said component of **HIV** is vif.

63. The nucleic acid molecule of claim 1 or 2, wherein said component of **HIV** is tat.

64. The nucleic acid molecule of claim 1 or 2, wherein said component of **HIV** is rev.

65. The nucleic acid molecule of claim 1 or 2, wherein said component of **HIV** is LTR.

66. The nucleic acid molecule of claim 65, wherein said LTR is the 3'-LTR.

67. The nucleic acid molecule of claim 65, wherein said LTR is the 5'-LTR.

68. A method of administering to a cell a nucleic acid molecule of any of claims 1-5 comprising contacting said cell with the nucleic acid molecule under conditions suitable for said administration.

69. The method of claim 68, wherein said cell is a mammalian cell.

70. The method of claim 68, wherein said cell is a human cell.

71. The method of claim 68, wherein said administration is in the presence of a delivery reagent.

72. The method of claim 71, wherein said delivery reagent is a lipid.

73. The method of claim 72, wherein said lipid is a cationic lipid.

74. The method of claim 72, wherein said lipid is a phospholipid.

75. The method of claim 71, wherein said delivery reagent is a liposome.

L11 ANSWER 10 OF 21 USPATFULL on STN
2003:137157 Lentivirus from the group of immunodeficiency viruses of drill monkeys (Mandrillus leucophaeus) and their use.
Guertler, Lutz Gerhard, Greifswald, GERMANY, FEDERAL REPUBLIC OF
Hauser, Hans Peter, Marburg, GERMANY, FEDERAL REPUBLIC OF
Dongmo Deloko, Yvette Beatrice, Munich, GERMANY, FEDERAL REPUBLIC OF
Zekeng, Leopold, Cameroon, AFRICAN INTELLECTUAL PROPERTY ORGANIZATION (OAPI)
Kaptue, Lazare, Cameroon, AFRICAN INTELLECTUAL PROPERTY ORGANIZATION (OAPI)
Dade Behring Marburg GmbH, GERMANY, FEDERAL REPUBLIC OF (non-U.S. corporation)
US 6566513 B1 20030520
APPLICATION: US 2000-625972 20000726 (9)
PRIORITY: DE 1999-19936003 19990803
DOCUMENT TYPE: Utility; GRANTED.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to an immunodeficiency virus of drill monkeys, its RNA, the corresponding cDNA, proteins derived therefrom and fragments of the nucleic acids or proteins. The invention likewise relates to the diagnostic use of the nucleic acids and proteins mentioned and their fragments and to a diagnostic.
CLM What is claimed is:
1. An isolated and purified nucleic acid molecule comprising SEQ ID NO: 21.

2. An isolated immunodeficiency virus comprising SEQ ID NO: 21.

3. The virus of claim 2, further comprising a nucleic acid molecule selected from the group consisting of SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO; 20 and SEQ ID NO: 22.

4. An isolated immunodeficiency virus comprising SEQ ID NO: 21 or a variant thereof, wherein said variant encodes SEQ ID NO: 26, wherein the arginine or lysine in position 3 is substituted with a different amino

acid.

5. An isolated immunodeficiency virus of claim 4, wherein said different amino acid is a polar amino acid or an amino acid having an aliphatic side chain.

6. The isolated immunodeficiency virus of claim 5, wherein said polar amino acid is serine and said amino acid having an aliphatic side chain is alanine.

L11 ANSWER 11 OF 21 USPATFULL on STN
2003:71319 Nucleotide sequences of **HIV**-1 group (or subgroup) O retroviral antigens.
Charneau, Pierre, Paris, FRANCE
Clavel, Francois, Paris, FRANCE
Borman, Andrew, Villemeux-Sur-Eure, FRANCE
Quillent, Caroline, Vitry-Sur-Seine, FRANCE
Guetard, Denise, Paris, FRANCE
Montagnier, Luc, Le Plessis-Robinson, FRANCE
Saint-Martin, Jacqueline Donjon De, Clamart, FRANCE
Cohen, Jacques H.M., Reims, FRANCE
Institut Pasteur (non-U.S. corporation)
US 2003049604 A1 20030313
APPLICATION: US 2001-26741 A1 20011227 (10)
PRIORITY: FR 1994-12554 19941020
FR 1995-2526 19950303
DOCUMENT TYPE: Utility; APPLICATION.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB An **HIV**-1 type (or subtype) O retrovirus protein, or a natural or synthetic polypeptide or peptide including at least a part of said protein, which is capable of being recognised by antibodies isolated from a serum resulting from infection by an **HIV**-1 type O VAU strain or an **HIV**-1 type (or subtype) O DUR strain.
CLM What is claimed is:
1. **HIV**-1 group (or subgroup) O retroviral protein, or natural or synthetic peptide or polypeptide comprising at least a part of said protein, which is capable of being recognized by antibodies which may be isolated from serum obtained after an infection with an **HIV**-1 group O VAU strain, or an **HIV**-1 group (or subgroup) O DUR strain.

2. Protein, polypeptide or peptide according to claim 1, characterized in that it may be obtained by expression, in a host cell, of a nucleotide sequence, more particularly DNA and cloned DNA fragments which may be obtained from RNA, from cDNA or from primers which may be used for gene amplification, derived from RNA or from DNA of the **HIV**-1 group (or subgroup) O retrovirus, said nucleotide sequence being characterized in that it comprises the sequence corresponding to Seq ID No. 5 as well as any portion of that sequence or variant of that portion which is capable of hybridizing with the corresponding DNA or RNA of the **HIV**-1 group (or subgroup) O virus, and in that said protein comprises the amino acid sequence between residues 1 and 526 of Seq ID No. 6 as well as any peptide, polypeptide, glycoprotein or variant derived from said sequence having an epitope which may be recognized by antibodies induced by the **HIV**-1(VAU) virus.

3. Protein, polypeptide or peptide according to claim 1 or 2, characterized in that it may be obtained by expression, in a host cell, of a nucleotide sequence according to claim 1, and in that said protein comprises the amino acid sequence between residues 527 to 877 of Seq ID No. 7 as well as any peptide, polypeptide, glycoprotein or variant derived from said sequence having an epitope which may be recognized by antibodies induced by the **HIV**-1(VAU) virus.

4. Peptide or polypeptide according to claim 1 to 3, characterized in that it comprises the sequence CKNRLIC or in particular the sequence

RLLALETFIQNWWLLNLWGCKNRLIC or a variant of that sequence such as the sequence RLWALETLIQNQQRLNLWGCKGKLIC, the sequence RLLALETLLQNQQLLSLWGCKGKLVC, the sequence RARLLALETFIQNQQLLNLWGCKNRLICYTS VKWNKT, the sequence CERPGNQKIMAGPMAWYS MALSNTKGDTRAAYC or the sequence GPMAWY.

5. Synthetic peptide, characterized in that it is a protein fragment according to one of claims 1 to 4, in that it is obtained from the sequence SEQ ID No. 6 or from the sequence SEQ ID No. 7 and in that it is recognized by antibodies induced against an **HIV**-1(VAU) retrovirus or variant of this fragment capable of being recognized by antibodies induced by an **HIV**-1(VAU) retrovirus.

6. Protein, polypeptide or peptide according to claim 1, characterized in that said protein is a protein of the **HIV**-1 group (or subgroup) O(DUR) virus, deposited on Feb. 23, 1995 at the CNCM under the reference I-1542 or a natural or synthetic peptide or polypeptide comprising at least a part of said protein or a peptide whose sequence is distinguished from that of the above by substitution, deletion or addition of amino acids, this separate peptide nevertheless retaining the antigenic characteristics of the above one.

7. Peptide according to claim 6, containing at least 4 consecutive amino acids whose entire consecutive amino acid sequence is contained in the GAG sequence represented in FIG. 8 or in an immuno-logically similar GAG sequence obtained from a variant of the **HIV**-1 group (or subgroup) O DUR virus, said immunologically similar sequence being recognized by antibodies which also specifically recognize at least one of the sequences AHPQQA, LWTTRAGNP contained in the GAG sequence of FIG. 8.

8. Peptide according to claim 7, characterized in that it consists of a peptide whose amino acid sequence is contained either in one of the following sequences:

SPRTLNAWVKAVEEKAFNPEIIPMFMALSEGA (1)

MLNATGGHQGALQVLKEVIN (2)

GPLPPGQIREPTGSDIAGTTSTQQEQI (3)

IPVGDIYRKWIVLGLNKMVKMYSPVSILDI (4)

QGPKEPFRDYVDRFYKTKLAE (5)

AHPQQA (5a)

LWTTRAGNP (5b) or in the corresponding immunologically similar sequence, this peptide containing at least 4 consecutive amino acids of one of said sequences.

9. Peptide according to claim 8, characterized in that it consists of a peptide whose amino acid sequence is contained either in one of the following sequences:

SPRTLNAWVK (6)

GSDIAGTTST (7)

QGPKEPFRDYVDRF (8)

or in the corresponding immunologically similar sequence, this peptide containing at least four consecutive amino acids of one of said sequences.

10. Peptide according to claim 8, characterized in that it contains the following amino acid sequence: NPEI (9).

11. Peptide according to claim 8, characterized in that it contains the following amino acid sequence: AVEEKAFNPEIIPMFM (10).

12. Peptide according to claim 6, containing at least 4 consecutive amino acids, whose entire sequence is contained in the sequence of the region of the V3 loop of gp120 represented in FIG. 9 or in the corresponding immunologically similar sequence, obtained from a variant of the **HIV**-1 group (or subgroup) O DUR virus, said immunologically similar sequence being recognized by antibodies which also specifically recognize at least one of the sequences:

KEIKI (12)

EREGKGAN (13),

CVRPGNNSVKEIKI (14),

QIEREGKGANSR (15).

13. Peptide according to claim 12, containing: a) either the sequence CVRPGNNSVKEIKIGPMAWYSMQIEREGKGANSRTAFC (11) or a part of this sequence which contains at least 4 amino acids b) or an amino acid sequence which is separate from the sequence of a) in which one or more amino acids are replaced with two amino acids, with the proviso that the peptide retains its reactivity with an antiserum against the above said peptide, c) or an amino acid sequence which is separate from a) or b), in which one or more amino acids have been deleted or added, with the proviso that the peptide retains its reactivity with an antiserum against the peptide of a), d) or the corresponding immunologically similar sequence or part of sequence.

14. Peptide according to claim 13, which contains the sequence KEIKI (12).

15. Peptide according to claim 13, which contains the sequence EREGKGAN (13).

16. Peptide according to claim 13 or 14, which contains either the amino acid sequence CVRPGNNSVKEIKI (14) or the sequence QIEREGKGANSR (15).

17. Peptide according to claim 13, which comprises the sequence GPMAWYSM (16).

18. Peptide according to claim 6, containing at least 4 consecutive amino acids, whose entire sequence is contained in the sequence of the immunodominant region of gp41 represented in FIG. 9 or in the corresponding immunologically similar sequence, obtained from a variant of the **HIV**-1 group (or subgroup) O DUR virus, said immunologically similar sequence being recognized by antibodies which also specifically recognize at least one of the sequences:

RLLALETLMQNQQL (17),

LNLWGCRGKAICYTSVQWNETWG (18),

CRGKAI (19),

SVQWN (20),

RLLALETLMONQQLLNLWGCRGKAICYTS (21),

QNQQLLNLWGCRGKAICYTSVQWN (22).

19. Peptide according to claim 18, containing the sequence RLLALETLMQNQQL (17) LNLWGCRGKAICYTSVQWNETWG (18) or part of this peptide

containing: a) either the sequence CRGKAI (19) or the sequence SVQWN (20) in which Q is, where appropriate, replaced by a different amino acid, which is nevertheless also different from K, or the two sequences at the same time, b) or an amino acid sequence which is separate from the sequence of a) in which one or more amino acids are replaced with two amino acids, with the proviso that the peptide retains its reactivity with an antiserum against the peptide of a), c) or an amino acid sequence which is separate from a) or b), in which one or more amino acids have been deleted or added, with the proviso that the peptide retains its reactivity with an antiserum against the peptide of a), d) or in the corresponding immunologically similar sequence or part of sequence.

20. Peptide according to claim 19, characterized in that its N-terminal sequence which contains at least 8 amino acids is not immunologically recognized by antibodies formed against the sequence RILAVERY contained in the immunodominant region of gp41 of the **HIV**-1-LAI strain.

21. Peptide according to claim 19, characterized in that it is not recognized by antibodies formed against the peptide SGKLIC of the **HIV**-1-LAI strain.

22. Peptide according to claim 19, characterized in that it contains one or the other of the following two sequences:

RLLALETLMONQQLLNLWGCRGKAICYTS (21)

QNQQLLNLWGCRGKAICYTSVQWN (22).

23. Nucleotide sequence, more particularly DNA and cloned DNA fragments which may be obtained from RNA, from cDNA or from primers which may be used for gene amplification, derived from the RNA or the DNA of the **HIV**-1 group (or subgroup) O retrovirus, said nucleotide sequence being characterized in that it comprises the sequence corresponding to one of the sequences Seq ID No. 5, Seq ID No. 9, Seq ID No. 10 or Seq ID No. 11, as well as any portion of this sequence, in particular the sequences coding for the proteins, polypeptides or peptides of any one of claims 8 to 22 or variant of this portion which is capable of hybridizing with the corresponding DNA or RNA of the **HIV**-1 group (or subgroup) O virus.

24. Nucleotide sequence according to claim 23, characterized in that it is DNA or DNA fragments obtained from RNA, from cDNA or from primers for gene amplification, derived from the RNA or the DNA of the **HIV**-1(VAU) or **HIV**-1(DUR) retrovirus, the sequence comprising the sequence corresponding to Seq ID No. 5 as well as any portion of this sequence or variant of this portion which is capable of hybridizing with the corresponding DNA or RNA of the **HIV**-1(VAU) virus, or the sequence comprising the sequence corresponding to Seq ID No. 9 or Seq ID No. 10 or Seq ID No. 11, as well as any portion of this sequence or variant of this portion which is capable of hybridizing with the corresponding DNA or RNA of the **HIV**-1(DUR) virus.

25. Nucleotide sequence according to claim 23 or claim 7, characterized in that said sequence is chosen from the group of sequences corresponding to Seq ID No. 1, Seq ID No. 2, Seq ID No. 3 and Seq ID No. 4.

26. Nucleotide sequence, characterized in that it comprises the sequence of nucleotides corresponding to SEQ ID No. 7 and in that it codes for the integrase of an **HIV**-1 group (or subgroup) O retrovirus, in particular of an **HIV**-1(VAU) retrovirus, or nucleotide sequence which hybridizes with the sequence containing the sequence SEQ ID No. 7.

27. Oligonucleotide comprising at least 9 nucleotides, as obtained from a nucleotide sequence according to any one of claims 23 to 26, which is capable of being used as a primer for the gene amplification of an

HIV-1 group (or subgroup) O retrovirus.

28. Oligonucleotide according to claim 27, having a sequence consisting of at least nine consecutive nucleotides of the following nucleotide sequences:

ATT CCA ATA CAC TAT TGT GCT CCA-3'

AAA GAA TTC TCC ATG ACT GTT AAA-3'

GGT ATA GTG CAA CAG CAG GAC AAC-3'

AGA GGC CCA TTC ATC TAA CTC-3'

29. Oligonucleotide according to claim 28, characterized in that it may be used during a process of gene amplification of a nucleotide sequence coding for a peptide according to any one of claims 6 to 22.

30. Nucleotide sequence which may be used as a probe, characterized in that it hybridizes under highly stringent hybridization conditions with the DNA produced by gene amplification by means of primers according to any one of claims 27 to 29.

31. Composition for the detection of the presence or absence of an **HIV**-1 group (or subgroup) O retrovirus, in particular the **HIV**-1(VAU) and/or **HIV**-1(DUR) retrovirus, in samples of serum or of other biological liquids or tissue obtained from patients suspected of being carriers of an **HIV**-1 group (or subgroup) O retrovirus, said composition being characterized in that it comprises at least one probe obtained from a nucleotide sequence derived from the genome of the **HIV**-1(VAU) virus, particularly an **HIV**-1(VAU) DNA fragment containing the env region or a part of the env region of the **HIV**-1(VAU) virus, of a variant of **HIV**-1(VAU) as defined in any one of claims 23 to 27, and/or a probe obtained from a nucleotide sequence derived from the genome of the **HIV**-1(DUR) virus, the **HIV**-1(DUR) DNA containing the env region or a part of the env region and a part of the GAG region of the **HIV**-1(DUR) virus as defined [lacuna] claim 23 or 24.

32. Composition according to claim 12, characterized in that said composition also comprises a probe obtained from a nucleotide sequence obtained from **HIV**-1 not belonging to the O subgroup and/or from **HIV**-2.

33. Composition for the detection of the presence or absence of an **HIV**-1 group (or subgroup) O retrovirus, in particular the **HIV**-1(VAU) retrovirus and/or the **HIV**-1 group (or subgroup) O(DUR) retrovirus in a biological sample, said composition being characterized in that it comprises at least two nucleotide sequences according to any one of claims 23 to 27, and at least two nucleotide sequences according to claim 23 or 24, which are respectively derived from the genome of the **HIV**-1(VAU) and **HIV**-1(DUR) viruses, which sequences can be used as primers for amplification, in particular by PCR, of the DNA and/or the RNA of **HIV**-1 retrovirus of the O subgroup and in particular of **HIV**-1(VAU) and **HIV**-1(DUR).

34. Nucleotide sequence, characterized in that it is an RNA sequence corresponding to a DNA sequence according to any one of claims 23 to 31.

35. Composition for the in vitro detection of the presence, in a human biological sample, of anti-**HIV**-1(VAU) and anti-**HIV**-1(DUR) antibodies, said composition comprising at least one antigen comprising a protein, a glycoprotein, a polypeptide or a peptide of the envelope protein of an **HIV**-1(VAU) retrovirus as defined in any one of claims 1 to 5 and/or of the sequence comprising the sequence corresponding to Seq ID No. 9 or Seq ID No. 10 or Seq ID No. 11, as well as any portion of this sequence or variant of this portion which is

capable of hybridizing with the corresponding DNA or RNA of the **HIV**-1(DUR) virus.

36. Composition according to claim 35, characterized in that it also comprises an antigen such as a protein, a glycoprotein, a polypeptide or a peptide of an **HIV**-1 virus not belonging to the subgroup O and/or of an **HIV**-2 virus or a peptide derived from an **HIV**-1 virus not belonging to the subgroup O and/or of an **HIV**-2 virus having an epitope which may be recognized by the antibodies induced by the **HIV**-1 virus not belonging to the subgroup O and/or the **HIV**-2 virus.

37. Composition according to claim 36, characterized in that the proteins and/or glycoproteins of **HIV**-1 not belonging to the subgroup O and/or of **HIV**-2 are gag or pol proteins or peptides thereof.

38. Composition according to claim 37, characterized in that the proteins and/or glycoproteins of **HIV**-1 not belonging to the subgroup O and/or of **HIV**-2 are envelope glycoproteins.

39. Composition according to any one of claims 35 to 38, characterized in that said composition comprises a peptide sequence corresponding to the entire region 590-620 of the gp41 protein of **HIV**-1(VAU) or a part of this region which is specific for **HIV**-1(VAU).

40. Composition according to claim 20, characterized in that said peptide sequence is the sequence -TFIQN-, CKNRLIC or WGCKNR.

41. Antibody which may recognize a protein, a peptide or a polypeptide derived from said protein according to any one of claims 1 to 22.

42. Process for the in vitro diagnosis of an infection caused by the **HIV**-1(VAU) virus and/or by the **HIV**-1(DUR) virus, said process comprising: the placing in contact of a serum or of another biological medium, derived from a patient forming the subject of the diagnosis, with at least one of the envelope proteins or glycoproteins of the **HIV**-1(VAU) and/or **HIV**-1(DUR) virus or of a peptide or polypeptide obtained from one of these proteins or glycoproteins respectively according to any one of claims 1 to 5 and according to any one of claims 6 to 22, or a composition according to any one of claims 35 to 38, and the detection of an immunological reaction.

43. Reagent required for the Western blot (immunoblot) or ELISA reaction, containing an envelope protein or glycoprotein of the **HIV**-1(VAU) and/or **HIV**-1(DUR) virus or of a peptide or polypeptide obtained from one of these proteins or glycoproteins according to any one of claims 1 to 5 and according to any one of claims 6 to 22 or a composition according to any one of claims 35 to 38.

44. Use of a nucleotide sequence according to claim 23 or 24 in order to induce in vivo the synthesis of antibodies directed against the antigen coded for by said sequence.

45. Immunogenic composition according to any one of claims 35 to 38, which is capable of inducing antibodies in animals.

46. Diagnostic kit for the in vitro detection, on a biological sample, of an infection with an **HIV**-1 subgroup O retrovirus, for example of an **HIV**-1(VAU) and/or **HIV**-1(DUR) retrovirus, characterized in that it comprises: primers according to any one of claims 27 to 29 for the gene amplification of an **HIV**-1 subgroup O retrovirus, reagents required for the gene amplification reaction.

47. Kit for the in vitro detection, on a biological sample, of an **HIV**-1 subgroup O retrovirus, characterized in that it comprises as optionally labeled probe, at least one nucleotide sequence according to one of claims 23 to 29 and 34 or a composition according to one of

claims 31, 32 or 33, and optionally another nucleotide probe according to any one of claims 23 to 29 or composition according to any one of claims 31, 32 or 33, which is optionally immobilized on a solid support.

48. Kit according to claim 28, characterized in that it also comprises the reagents required for carrying out a hybridization.

49. Process of detection and discrimination, in a biological sample, between antibodies characteristic of an **HIV**-1 group (or subgroup) O retrovirus and antibodies characteristic of an **HIV**-1 subgroup M retrovirus, characterized by the placing in contact of this biological sample with a peptide chosen from peptides (1), (2), (3), (4), (5a) and (5b) of claim 8, peptide (9) of claim 10 and peptide (10) of claim 11.

50. Process of detection and discrimination, in a biological sample, between antibodies characteristic of an **HIV**-1 group (or subgroup) O retrovirus and antibodies characteristic of an **HIV**-1 subgroup M retrovirus, characterized by the placing in contact of this biological sample with a peptide obtained from one of the **HIV**-1 subgroup M viruses taken into consideration in FIGS. 8 and 9 and homologous with a peptide chosen from those of claim 49, the sequence of this homologous peptide resulting from vertical alignments of its own successive amino acids, which are themselves contained in the pertinent peptide sequence relative to the corresponding **HIV**-1 subgroup M virus and represented in FIG. 8 or 9 with the successive amino acids of the chosen peptide sequence, as also follows from FIG. 8 or 9.

51. Process of detection and discrimination between infection with an **HIV**-1 group (or subgroup) O retrovirus and of the **HIV**-1 subgroup M type, characterized by the placing in contact of sera, derived from individuals subjected to a diagnostic test for AIDS, with the peptide RILAVERY.

52. Process for the detection of infection due either to an **HIV**-1 group (or subgroup) O or **HIV**-1 subgroup M retrovirus, characterized by the use of mixtures of two categories of peptides, those of the first category corresponding to those identified in claim 49.

53. Process of discrimination between an infection due to an **HIV**-1 group (or subgroup) O DUR retrovirus or variant, and an infection due to another type of **HIV**-1 group (or subgroup) O retrovirus, characterized by the placing in contact of the biological sample studied with any one of the following peptides: peptide (11) of claim 38, peptide (12) of claim 39 or peptide (13) of claim 40, peptide (14) or peptide (15) of claim 41 or peptides (17), (18), (19) and (20) of claim 44.

54. Vector containing a nucleic acid whose nucleotide sequence corresponds to any one of the sequences of claims 23 to 30.

55. Vector according to claim 57, characterized in that it is a plasmid.

56. Plasmid chosen from those which were deposited at the CNCM on Feb. 24, 1995 under the references I-1548, I-1549 and I-1550.

57. Cell containing a nucleic acid whose nucleotide sequence corresponds to any one of the sequences of claims 54 and 55.

58. Virus deposited on Feb. 23, 1995 at the CNCM under the reference I-1542.

59. Virus of the same type or subtype as the virus of claim 58, characterized in that the consensus peptides of this virus are recognized by antibodies which specifically recognize a peptide according to any one of claims 6 to 22.

60. Kit for the in vitro detection of antibodies against **HIV**,

containing at least one peptide according to any one of claims 6 to 22.

61. Kit according to claim 60, also containing at least one consensus peptide derived from another **HIV** strain comprising: either an amino acid sequence which is separate from the sequence of this peptide, in which one or more amino acids are replaced with other amino acids, with the proviso that the peptide retains its reactivity with an antiserum against the consensus peptide, or an amino acid sequence in which one or more amino acids have been deleted or added, with the proviso that the peptide or polypeptide retains its reactivity with an antiserum against the consensus peptide.

62. Kit according to claim 60 or 61, characterized in that the other **HIV** strain is an **HIV**-LAI strain.

63. Process of discrimination between an infection with an **HIV**-1 group (or subgroup) O retrovirus and an **HIV**-1 subgroup M retrovirus, using a serine protease whose cleaving action is carried out on an SR dipeptide, and comprising the detection of a cleavage or of a on-cleavage of the V3 loop of gp120 of the retrovirus, depending on whether this retrovirus is an **HIV**-1 group (or subgroup) O retrovirus or an **HIV**-1 subgroup M retrovirus.

64. Viral lysate as obtained by lysis of cells infected with a virus according to claim 58 or 59 or with an **HIV**-1(VAU) virus.

65. Protein extract of **HIV**-1 O(DUR) strain containing in particular an antigenic peptide according to any one of claims 6 to 22, or of **HIV**-1 group (or subgroup) O(VAU) strain containing in particular an antigenic peptide according to any one of claims 1 to 5.

66. Bacterial strain deposited at the CCNM on Oct. 20, 1994 under the access number I-1486.

67. Composition for detection and discrimination, in a biological sample, between an **HIV**-1 subgroup M retrovirus and an **HIV**-1 group (or subgroup) O retrovirus, comprising a mixture of two categories of peptides, the first being those identified in claim 49.

68. Peptide according to claim 8, characterized in that it consists of a peptide whose amino acid sequence is contained either in one of the following sequences:

IGGHQGALQ (23)

REPTGSDI (24)

or in a corresponding immunologically similar sequence, this peptide containing at least 4 consecutive amino acids of one of said sequences.

69. Peptide according to claim 7, characterized in that it consists of a peptide whose amino acid sequence is contained in the following amino acid sequence: INDEAADWD (25) or in a corresponding immunologically similar sequence, this peptide containing at least 4 consecutive amino acids of said sequence.

70. Nucleic acid coding for the peptides of claims 68 and 69.

71. Composition comprising at least one nucleic acid according to claim 70.

72. Use of at least one nucleic acid according to claims 70 and 71 for detection and discrimination between **HIV**-1 group M and **HIV**-1 group O strains.

L11 ANSWER 12 OF 21 USPATFULL on STN
2003:47837 Complete genome sequence of a simian immunodeficiency virus from a red-capped mangabey.
Hahn, Beatrice H., Birmingham, AL, United States
Gao, Feng, Hoover, AL, United States
Shaw, George M., Birmingham, AL, United States
Marx, Preston A., Covington, LA, United States
Smith, Stephen M., Essex Fells, NJ, United States
Georges-Courbot, Marie Claude, Paris, FRANCE
Lu, Chang Yong, Forest Hills, NY, United States
UAB Research Foundation, Birmingham, AL, United States (U.S. corporation)
US 6521739 B1 20030218
APPLICATION: US 1998-206551 19981207 (9)
DOCUMENT TYPE: Utility; GRANTED.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The nucleotide sequence and deduced amino acid sequences of the complete genome of a simian immunodeficiency virus isolate from a red-capped mangabey are disclosed. The invention relates to the nucleic acids and peptides encoded by and/or derived from these sequences and their use in diagnostic methods and as immunogens.
CLM What is claimed is:
1. An isolated and purified polypeptide encoded by nucleic acid comprising the nucleotide sequence of the genome of the simian immunodeficiency virus isolate SIVrcm shown in SEQ ID NO: 1, wherein the amino acid sequence of said polypeptide comprises a sequence selected from the group consisting of SEQ ID NO: 10, 23, 45-53, 54 and 56.

2. A composition comprising the isolated and purified polypeptide of claim 1 and a physiologically acceptable carrier.

L11 ANSWER 13 OF 21 USPATFULL on STN
2003:26241 **HIV**-1 group O antigens and uses thereof.
DeLaporte, Eric, Saint Jean de Cuculles, FRANCE
Peeters, Martine, Saint Jean de Cuculles, FRANCE
Saman, Eric, Bornem, BELGIUM
Vanden Haesevelde, Marleen, Oudenaarde, BELGIUM
Innogenetics, N.V., BELGIUM (non-U.S. corporation)
US 6511801 B1 20030128
WO 9904011 19990128
APPLICATION: US 2000-462917 20000403 (9)
WO 1998-EP4522 19980720
PRIORITY: EP 1997-870110 19970718
DOCUMENT TYPE: Utility; GRANTED.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The claimed invention relates to an **HIV**-1 group O envelope antigen comprising SEQ ID NO: 100, and the use of said antigen as a reagent in the diagnosis of **HIV**-1 group O infection, and a kit therefore.
CLM What is claimed is:
1. An isolated antigen from the **HIV**-1 group O strain gp160 env precursor protein comprising the amino acid sequence of SEQ ID NO:100.

2. A method for detecting anti-**HIV**-1 antibodies in a sample comprising: a) contacting the sample with an isolated antigen from the **HIV**-1 group O strain gp160 env precursor protein comprising the amino acid sequence of SEQ ID NO:100, b) allowing the isolated antigen and anti-**HIV** antibodies to interact, and c) detecting the interaction between the antigen and the anti-**HIV** antibodies.

3. A kit for detecting **HIV**-1 antibodies comprising an isolated antigen from the **HIV**-1 group O strain gp160 env precursor protein comprising the amino acid sequence of SEQ ID NO:100.

4. An immunogenic composition comprising: a) an isolated antigen from the **HIV**-1 group O strain gp160 env precursor protein which comprises the amino acid sequence of SEQ ID NO:100; and b) a pharmaceutically

acceptable carrier.

L11 ANSWER 14 OF 21 USPATFULL on STN
2003:20024 Non-M non-O **HIV** strains, fragments and uses.
Mauclere, Phillippe, Bordeaux, FRANCE
Loussert-Ajaka, Ibtissam, Sartrouville, FRANCE
Simon, Francois, Paris, FRANCE
Saragosti, Sentob, Billancourt, FRANCE
Barre-Sinoussi, Francoise, Moulimeaux, FRANCE
Institute National de la Sante et de la Recherche Medicale-Inserm, Paris, FRANCE (non-U.S. corporation)
US 6509018 B1 20030121
WO 9826075 19980618
APPLICATION: US 1999-319588 19990827 (9)
WO 1997-FR2227 19971208
PRIORITY: FR 1996-15087 19961209
DOCUMENT TYPE: Utility; GRANTED.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention provides peptides which are expressed by the env gene of a non-M, non-O **HIV**-1 virus, in particular a strain designated YBF30. The invention also provides fragments of the peptides that including the V3 loop region and their corresponding nucleotide sequences. The invention further provides kits including diagnostic reagents containing these molecules or immunogenic compositions containing these peptides, as well as methods for screening and typing non-M, non-O **HIV**-1 viruses and **HIV**-1 viruses expressing these peptide and/or nucleotide sequences.
CLM What is claimed is:
1. An isolated peptide comprising SEQ ID NO: 58.

2. A peptide of claim 1, comprising SEQ ID NO: 18.

3. An isolated peptide expressed by the env gene comprising a sequence encoding SEQ ID NO: 58.

4. A peptide of claim 3, wherein the env gene is of a non-M, non-O **HIV**-1 strain exhibiting morphological and immunological characteristics of the retrovirus designated YBF30 and deposited as CNCM No. 1-1753.

5. A peptide of claim 3, wherein the peptide comprises SEQ ID NO: 18.

6. A peptide of claim 3, wherein the peptide comprises a V3 loop.

7. An isolated peptide consisting of SEQ ID NO: 58.

8. An isolated peptide expressed by the env gene of a non-M, non-O **HIV**-1 strain comprising SEQ ID NO: 58, wherein the peptide exhibits antibody-recognition capacity and can be recognized by antibodies which are induced by a non-M, non-O **HIV**-1 virus and which are present in a biological sample obtained following an infection with a non-M, non-O **HIV**-1 strain.

9. An immunogenic composition comprising an isolated peptide comprising SEQ ID NO: 18 or 58.

10. A kit for detecting a non-M, non-O **HIV**-1 virus, comprising at least one of the peptides of any one of claims 1 to 8.

L11 ANSWER 15 OF 21 USPATFULL on STN
2002:129714 Nucleotide sequences of **HIV**-1 type (or subtype) O retrovirus antigens.
Charneau, Pierre, Paris, FRANCE
Clavel, Fran.cedilla.ois, Paris, FRANCE
Borman, Andrew, Villemeux-sur-Eure, FRANCE

Quillent, Caroline, Vitry sur Seine, FRANCE
Guetard, Denise, Paris, FRANCE
Montagnier, Luc, Le Plessis-Robinson, FRANCE
Donjon De Saint-Martin, Jacqueline, Clamart, FRANCE
Cohen, Jacques, Reims, FRANCE
Institut Pasteur, Paris, FRANCE (non-U.S. corporation)
US 6399294 B1 20020604
WO 9612809 19960502
APPLICATION: US 1997-817441 19970711 (8)
WO 1995-FR1391 19951020 19970711 PCT 371 date
PRIORITY: FR 1994-12554 19941020
FR 1995-2526 19950303
DOCUMENT TYPE: Utility; GRANTED.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB An **HIV**-1 type (or subtype) O retrovirus protein, or a natural or synthetic polypeptide or peptide including at least a part of said protein, which is capable of being recognised by antibodies isolated from a serum resulting from infection by an **HIV**-1 type O VAU strain or an **HIV**-1 type (or subtype) O DUR strain.

CLM What is claimed is:

1. A purified **HIV**-1 DUR isolate, which is the isolate deposited at C.N.C.M. under the accession no. I-1542.

2. A purified nucleic acid comprising the sequence of SEQ ID NO:63.

3. A purified nucleic acid comprising the sequence of SEQ ID NO:64.

4. A purified **HIV**-1 Env peptide comprising a sequence selected from the group consisting of: CysValArgProGlyAsnAsnSerValLysGluIleLysIleGlyProMetAlaTrpTyrSerMetGlnIleGluArgGluGlyLysGlyAlaAsnSerArgThrAlaPheCys (SEQ ID NO:93); CysLysAsnArgLeuIleCys (SEQ ID NO:5); ArgLeuLeuAlaLeuGluThrPheIleGlnAsnTrpTrpLeuLeuAsnLeuTrpGlyCysLysAsnArgLeuIleCys (SEQ ID NO:6); ArgAlaArgLeuLeuAlaLeuGluThrPheIleGlnAsnGlnGlnLeuLeuAsnLeuTrpGlyCysLysAsnArgLeuIleCysTyrThrSerValLysTrpAsnLysThr (SEQ ID NO:7); LysGluIleLysIle (SEQ ID NO:23); GluArgGluGlyLysGlyAlaAsn (SEQ ID NO:24); CysValArgProGlyAsnAsnSerValLysGluIleLysIle (SEQ ID NO:25); GlnIleGluArgGluGlyLysGlyAlaAsnSerArg (SEQ ID NO:26); ArgLeuLeuAlaLeuGluThrLeuMetGlnAsnGlnGlnLeu (SEQ ID NO:29); LeuAsnLeuTrpGlyCysArgGlyLysAlaIleCysTyrThrSerValGlnTrpAsnGluThrTrpGly (SEQ ID NO:30); CysArgGlyLysAlaIle (SEQ ID NO:31); SerValGlnTrpAsn (SEQ ID NO:32); ArgLeuLeuAlaLeuGluThrLeuMetGlnAsnGlnGlnLeuLeuAsnLeuTrpGlyCysArgGlyLysAlaIleCysTyrThrSer (SEQ ID NO:33); GlnAsnGlnGlnLeuLeuAsnLeuTrpGlyCysArgGlyLysAlaIleCysTyrThrSerValGlnTrpAsn (SEQ ID NO:34); ThrPheIleGlnAsn (SEQ ID NO:40); and TrpGlyCysLysAsnArg (SEQ ID NO:41).

5. An oligonucleotide primer selected from the group consisting of: ATTCCAATACACTATTGTGCTCCA (SEQ ID NO:42); AAAGAATTCTCCATGACTGTTAAA (SEQ ID NO:43); GGTATAGTGCAACAGCAGGACAAC (SEQ ID NO:44); AGAGGCCCATTCATCTAACTC (SEQ ID NO:45); and sequences complementary to these sequences.

6. A probe for **HIV** group O, wherein said probe is at least 90% identical to SEQ ID NO:63.

7. A purified **HIV**-1 isolate comprising Env protein, wherein said Env protein comprises a sequence selected from the group consisting of: CysValArgProGlyAsnAsnSerValLysGluIleLysIleGlyProMetAlaTrpTyrSerMetGlnIleGluArgGluGlyLysGlyAlaAsnSerArgThrAlaPheCys (SEQ ID NO:93); CysLysAsnArgLeuIleCys (SEQ ID NO:5); ArgLeuLeuAlaLeuGluThrPheIleGlnAsnTrpTrpLeuLeuAsnLeuTrpGlyCysLysAsnArgLeuIleCys (SEQ ID NO:6); ArgAlaArgLeuLeuAlaLeuGluThrPheIleGlnAsnGlnGlnLeuLeuAsnLeuTrpGlyCysLysAsnArgLeuIleCysTyrThrSerValLysTrpAsnLysThr (SEQ ID NO:7); LysGluIleLysIle (SEQ ID NO:23); GluArgGluGlyLysGlyAlaAsn (SEQ ID NO:24); CysValArgProGlyAsnAsnSerValLysGluIleLysIle (SEQ ID NO:25); GlnIleGluArgGluGlyLysGlyAlaAsnSerArg (SEQ ID NO:26); ArgLeuLeuAlaLeuGluThrLeuMetGlnAsnGlnGlnLeu (SEQ ID NO:29);

LeuAsnLeuTrpGlyCysArgGlyLysAlaIleCysTyrThrSerValGlnTrpAsnGluThrTrpGly (SEQ ID NO:30); CysArgGlyLysAlaIle (SEQ ID NO:31); SerValGlnTrpAsn (SEQ ID NO:32); ArgLeuLeuAlaLeuGluThrLeuMetGlnAsnGlnGlnLeuLeuAsnLeuTrpGlyCysArgGlyLysAlaIleCysTyrThrSer (SEQ ID NO:33); GlnAsnGlnGlnLeuLeuAsnLeuTrpGlyCysArgGlyLysAlaIleCysTyrThrSerValGlnTrpAsn (SEQ ID NO:34); ThrPheIleGlnAsn (SEQ ID NO:40); and TrpGlyCysLysAsnArg (SEQ ID NO:41).

8. A probe for **HIV** group O, wherein said probe encodes an Env peptide comprising a sequence selected from the group consisting of: CysValArgProGlyAsnAsnSerValLysGluIleLysIleGlyProMetAlaTrpTyrSerMetGlnIleGluArgGluGlyLysGlyAlaAsnSerArgThrAlaPheCys (SEQ ID NO:93); CysLysAsnArgLeuIleCys (SEQ ID NO:5); ArgLeuLeuAlaLeuGluThrPheIleGlnAsnTrpTrpLeuLeuAsnLeuTrpGlyCysLysAsnArgLeuIleCys (SEQ ID NO:6); ArgAlaArgLeuLeuAlaLeuGluThrPheIleGlnAsnGlnGlnLeuLeuAsnLeuTrpGlyCysLysAsnArgLeuIleCysTyrThrSerValLysTrpAsnLysThr (SEQ ID NO:7); LysGluIleLysIle (SEQ ID NO:23); GluArgGluGlyLysGlyAlaAsn (SEQ ID NO:24); CysValArgProGlyAsnAsnSerValLysGluIleLysIle (SEQ ID NO:25); GlnIleGluArgGluGlyLysGlyAlaAsnSerArg (SEQ ID NO:26); ArgLeuLeuAlaLeuGluThrLeuMetGlnAsnGlnGlnLeu (SEQ ID NO:29); LeuAsnLeuTrpGlyCysArgGlyLysAlaIleCysTyrThrSerValGlnTrpAsnGluThrTrpGly (SEQ ID NO:30); CysArgGlyLysAlaIle (SEQ ID NO:31); SerValGlnTrpAsn (SEQ ID NO:32); ArgLeuLeuAlaLeuGluThrLeuMetGlnAsnGlnGlnLeuLeuAsnLeuTrpGlyCysArgGlyLysAlaIleCysTyrThrSer (SEQ ID NO:33); GlnAsnGlnGlnLeuLeuAsnLeuTrpGlyCysArgGlyLysAlaIleCysTyrThrSerValGlnTrpAsn (SEQ ID NO:34); ThrPheIleGlnAsn (SEQ ID NO:40); and TrpGlyCysLysAsnArg (SEQ ID NO:41).

9. A purified **HIV**-1 env gene, wherein said gene encodes a polypeptide comprising a sequence selected from the group consisting of: CysValArgProGlyAsnAsnSerValLysGluIleLysIleGlyProMetAlaTrpTyrSerMetGlnIleGluArgGluGlyLysGlyAlaAsnSerArgThrAlaPheCys (SEQ ID NO:93); CysLysAsnArgLeuIleCys (SEQ ID NO:5); ArgLeuLeuAlaLeuGluThrPheIleGlnAsnTrpTrpLeuLeuAsnLeuTrpGlyCysLysAsnArgLeuIleCys (SEQ ID NO:6); ArgAlaArgLeuLeuAlaLeuGluThrPheIleGlnAsnGlnGlnLeuLeuAsnLeuTrpGlyCysLysAsnArgLeuIleCysTyrThrSerValLysTrpAsnLysThr (SEQ ID NO:7); LysGluIleLysIle (SEQ ID NO:23); GluArgGluGlyLysGlyAlaAsn (SEQ ID NO:24); CysValArgProGlyAsnAsnSerValLysGluIleLysIle (SEQ ID NO:25); GlnIleGluArgGluGlyLysGlyAlaAsnSerArg (SEQ ID NO:26); ArgLeuLeuAlaLeuGluThrLeuMetGlnAsnGlnGlnLeu (SEQ ID NO:29); LeuAsnLeuTrpGlyCysArgGlyLysAlaIleCysTyrThrSerValGlnTrpAsnGluThrTrpGly (SEQ ID NO:30); CysArgGlyLysAlaIle (SEQ ID NO:31); SerValGlnTrpAsn (SEQ ID NO:32); ArgLeuLeuAlaLeuGluThrLeuMetGlnAsnGlnGlnLeuLeuAsnLeuTrpGlyCysArgGlyLysAlaIleCysTyrThrSer (SEQ ID NO:33); GlnAsnGlnGlnLeuLeuAsnLeuTrpGlyCysArgGlyLysAlaIleCysTyrThrSerValGlnTrpAsn (SEQ ID NO:34); ThrPheIleGlnAsn (SEQ ID NO:40); and TrpGlyCysLysAsnArg (SEQ ID NO:41).

10. A purified **HIV**-1 nucleic acid, wherein said nucleic acid encodes a polypeptide comprising a sequence selected from the group consisting of: CysValArgProGlyAsnAsnSerValLysGluIleLysIleGlyProMetAlaTrpTyrSerMetGlnIleGluArgGluGlyLysGlyAlaAsnSerArgThrAlaPheCys (SEQ ID NO:93); CysLysAsnArgLeuIleCys (SEQ ID NO:5); ArgLeuLeuAlaLeuGluThrPheIleGlnAsnTrpTrpLeuLeuAsnLeuTrpGlyCysLysAsnArgLeuIleCys (SEQ ID NO:6); ArgAlaArgLeuLeuAlaLeuGluThrPheIleGlnAsnGlnGlnLeuLeuAsnLeuTrpGlyCysLysAsnArgLeuIleCysTyrThrSerValLysTrpAsnLysThr (SEQ ID NO:7); LysGluIleLysIle (SEQ ID NO:23); GluArgGluGlyLysGlyAlaAsn (SEQ ID NO:24); CysValArgProGlyAsnAsnSerValLysGluIleLysIle (SEQ ID NO:25); GlnIleGluArgGluGlyLysGlyAlaAsnSerArg (SEQ ID NO:26); ArgLeuLeuAlaLeuGluThrLeuMetGlnAsnGlnGlnLeu (SEQ ID NO:29); LeuAsnLeuTrpGlyCysArgGlyLysAlaIleCysTyrThrSerValGlnTrpAsnGluThrTrpGly (SEQ ID NO:30); CysArgGlyLysAlaIle (SEQ ID NO:31); SerValGlnTrpAsn (SEQ ID NO:32); ArgLeuLeuAlaLeuGluThrLeuMetGlnAsnGlnGlnLeuLeuAsnLeuTrpGlyCysArgGlyLysAlaIleCysTyrThrSer (SEQ ID NO:33); GlnAsnGlnGlnLeuLeuAsnLeuTrpGlyCysArgGlyLysAlaIleCysTyrThrSerValGlnTrpAsn (SEQ ID NO:34); ThrPheIleGlnAsn (SEQ ID NO:40); and TrpGlyCysLysAsnArg (SEQ ID NO:41).

11. A method for the in vitro diagnosis of an infection caused by an **HIV**-1(VAU) virus, said process comprising: (A) obtaining a

biological sample comprising antibodies; (B) contacting said sample with at least one peptide of claim 4; and (C) detecting the immunological complexes formed.

L11 ANSWER 16 OF 21 USPATFULL on STN
2001:152490 Anti-**HIV** peptides and proteins.
Kingsman, Alan J., Oxon, United Kingdom
Kingsman, Susan M., Oxon, United Kingdom
Cannon, Paula M., Los Angeles, CA, United States
Oxford Biomedica (UK) Limited, Oxford, United Kingdom (non-U.S. corporation)
US 6287572 B1 20010911
WO 9837089 19980827
APPLICATION: US 1999-367953 19990824 (9)
WO 1998-GB563 19980223 19990824 PCT 371 date 19990824 PCT 102(e) date
PRIORITY: GB 1997-3802 19970224
DOCUMENT TYPE: Utility; GRANTED.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB This invention relates to novel peptides and proteins and nucleic acids encoding them, which are useful against **HIV** infection. The peptides comprise an amino acid sequence of a part of the **HIV**-1 p17 protein or of the **HIV**-2 p16 protein, from amino acid residues 31 to 45 or from amino acid residues 41 to 55. The proteins are recombinant p16 and p17 proteins having an alteration in helix A which is defined by amino acid residues 31 to 46, or the A-B loop which is defined by amino acid residues 47 to 52.
CLM What is claimed is:
1. A recombinant p17 protein which is incapable of functioning as the natural protein as a result of substitution of amino acid residue A45.

2. A recombinant p17 protein which is incapable of functioning as the natural protein as a result of substitution of amino acid residues R39 or R43.

3. A recombinant p17 protein according to claims 1 or 2, which is a natural or engineered variant of the **HIV** protein, said variant containing one or more conservative amino acid substitutions.

4. A composition comprising a peptide of claims 1 or 2 with a carrier or diluent.

L11 ANSWER 17 OF 21 USPATFULL on STN
2001:125748 Group O **HIV**-1, fragments of such viruses, and uses thereof.
Simon, Fran.cedilla.ois, Paris, France
Saragosti, Sentob, Boulogne-Billancourt, France
Loussert-Ajaka, Ibtissam, Sartrouville, France
Ly, Thoai-Duong, Rueil-Malmaison, France
Chaix-Baudier, Marie-Laure, Paris, France
Institut National de la Sante et de la Recherche Medicale-Inserm, Paris, France (non-U.S. corporation)Assistance Publique-Hopitaux de Paris, Paris, France (non-U.S. corporation)
US 6270975 B1 20010807
APPLICATION: US 1999-444410 19991122 (9)
PRIORITY: FR 1995-2236 19950227
DOCUMENT TYPE: Utility; GRANTED.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Group **HIV**-1 retrovirus strains, particularly the strains known as BCF02, BCF01, BCF06, BCF07, BCF08, BCF11, BCF03, BCF09, BCF12, BCF13 and BCF14, fragments of said retroviruses, and the uses thereof as a diagnostic reagent and as an immunogen, are disclosed.
CLM What is claimed is:
1. An isolated nucleic acid obtained from a group of O **HIV**-1, wherein the sequence of said nucleic acid is selected from the group consisting of: SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ D NO:5, SEQ

ID NO:6, SEQ ID NO:7, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO: 14, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO: 18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, and SEQ ID NO:61.

2. A process for detecting a group of O **HIV**-1 comprising the steps: extracting **HIV**-1 nucleic acid material from a biological sample containing said **HIV**-1 nucleic acid; denaturing said **HIV**-1 nucleic acid; annealing said denatured **HIV**-1 nucleic acid with at least one nucleic acid as claimed in claim 1 to form a hybrid; extending the hybrid; detecting the extended hybrid.

3. The process of claim 2, wherein said biological sample is obtained from serum or circulating lymphocytes.

4. The process of claim 2, wherein said step of extending the hybrid comprises addition of DNA polymerase and deoxyribonucleic acids.

5. The process of claim 2, wherein after said extracting the nucleic acid is treated with reverse transcriptase.

6. A process for screening and typing group O **HIV**-1, comprising bringing any of the nucleotide fragments in accordance with claim 1 into contact with the nucleic acid of the virus to be typed and detecting the hybrid formed.

7. An in vitro diagnostic reagent for a group of O **HIV**-1, comprising a sequence according to claim 1.

8. An in vitro diagnostic reagent for a group of O **HIV**-1, wherein said diagnostic reagent is selected from the group consisting of SEQ ID NOS: 22, 23, 24, and 25, which sequences may be used as primers for the amplification of a gp41 fragment from a group O **HIV**-1 viruses.

L11 ANSWER 18 OF 21 USPATFULL on STN
2000:156965 Peptides for the detection of **HIV**-1 group O.
De Leys, Robert, Three Bridges, NJ, United States
Zheng, Jian, Raritan, NJ, United States
Ortho-Clinical Diagnostics, Inc., Rochester, NY, United States (U.S. corporation)
US 6149910 20001121
APPLICATION: US 1999-433428 19991104 (9)
DOCUMENT TYPE: Utility; Granted.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB This invention relates to peptides and their preparation. The peptides each have a sequence that corresponds to the immunodominant region of the **HIV**-1 group O gp41 envelope protein. The sequence is characterized in that it does not correspond to any known naturally occurring group O sequence or variant. Furthermore, the peptide binds anti-**HIV**-1 group O antibodies. There are several uses for the peptides, including the detection of antibodies produced in response to **HIV**-1 group O infection. The peptides may also be incorporated in mosaics and expressed recombinantly.
CLM What is claimed is:
1. A peptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:59
NQQRLNSWGCKGRIICYTSARWH,
SEQ ID NO;61
EQQRLNSWGCKGRIICYTSARWH,
SEQ ID NO:69
GRETLMQDQQRLNSWGCKGRIICYTSARWH,
SEQ ID NO:60
XQQRLNSWGCKGRIICYTSARWH,

SEQ ID NO:62
ETLMQXQQRLNSWGCKGRIICYTSARWH,
SEQ ID NO:64
RARLQALETLMQNQQRLNSWGCKGRIICYTSARWH, and
SEQ ID NO:65
DQQVNNVSSIIYDKILEAQDQQEENVRELLELD.

2. The peptide of claim 1 wherein said peptide binds anti-**HIV** group O antibodies.

3. The peptide of claim 1 wherein said peptide is made by recombinant or synthetic chemistry methods.

L11 ANSWER 19 OF 21 USPATFULL on STN
2000:24443 Group O **HIV**-1, fragments of such viruses, and uses thereof.
Simon, Fran.cedilla.ois, Paris, France
Saragosti, Sentob, Boulogne-Billancourt, France
Loussert-Ajaka, Ibtissam, Sartrouville, France
Ly, Thoai-Duong, Rueil-Malmaison, France
Chaix-Baudier, Marie-Laure, Paris, France
Institut National de la Sante et de la Recherche Medical-Inserm, Paris Cedex, France (non-U.S. corporation)Assistance Publique-Hopitaux de Paris, Paris, France (non-U.S. corporation)
US 6030769 20000229
WO 9627013 19960906
APPLICATION: US 1997-894699 19971201 (8)
WO 1996-FR294 19960226 19971201 PCT 371 date 19971201 PCT 102(e) date
PRIORITY: FR 1995-2236 19950227
DOCUMENT TYPE: Utility; Granted.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Group **HIV**-1 retrovirus strains, particularly the strains known as BCF02, BCF01, BCF06, BCF07, BCF08, BCF11, BCF03, BCF09, BCF12, BCF13 and BCF14, fragments of said retroviruses, and the uses thereof as a diagnostic reagent and as an immunogen, are disclosed.
CLM What is claimed is:
1. A Group O **HIV**-1 strain having the morphological and immunological characteristics of a retrovirus selected from the group consisting of I-1543, I-1544, I-1545, I-1546 and I-1547.

2. The Group O **HIV**-1 strain comprising at least one sequence selected from the group consisting of: SEQ ID NO:1 to 7, SEQ ID NO:8 to 14 to SEQ ID NO: 15 to 21, SEQ ID NO:50 to 53, SEQ ID NO:54 to 57 and SEQ ID NO:58 to 61.

3. The strain of claim 2, which comprises SEQ ID NO:50, SEQ ID NO:54 and SEQ ID NO:58.

4. The strain of claim 2, which comprises SEQ ID NO:51, SEQ ID NO:55 and SEQ ID NO:59.

5. The strain of claim 2, which comprises SEQ ID NO:52, SEQ ID NO:56 and SEQ ID NO:60.

6. The strain of claim 2, which comprises SEQ ID NO:53, SEQ ID NO:57 and SEQ ID NO:61.

7. The strain of claim 2, which comprises SEQ ID NO:7, SEQ ID NO:14 and SEQ ID NO:21.

8. The strain of claim 2, which comprises SEQ ID NO:4, SEQ ID NO:11 and SEQ ID NO:18.

9. The strain of claim 2, which comprises SEQ ID NO:1, SEQ ID NO:8 and SEQ ID NO:15.

10. The strain of claim 2, which comprises SEQ ID NO:2, SEQ ID NO:9 and SEQ ID NO:16.

11. The strain of claim 2, which comprises SEQ ID NO:3, SEQ ID NO:10 and SEQ ID NO:17.

12. The strain of claim 2, which comprises SEQ ID NO:5, SEQ ID NO:12 and SEQ ID NO:19.

13. The strain of claim 2, which comprises SEQ ID NO:6, SEQ ID NO:13 and SEQ ID NO:20.

14. A peptide which is expressed by a Group O **HIV**-1 strain of claim 1.

15. A peptide which is expressed by a Group O **HIV**-1 strain of claim 2.

16. A peptide selected from the group consisting of: SEQ ID NO:26 to 35, SEQ ID NO:36 to 42, SEQ ID NO:43 to 49, SEQ ID NO:62 to 65, SEQ ID NO:66 to 69, SEQ ID NO:70 to 72 and SEQ ID NO:73.

17. An immunogenic composition, comprising a peptide of claim 14.

18. An immunogenic composition, comprising a peptide of claim 15.

19. An immunogenic composition, comprising one or more products of translation of the sequences of claim 10.

20. An antibody which binds to a peptide of claim 14.

21. An antibody which binds to a peptide of claim 15.

22. A method of in vitro diagnosis of a Group O **HIV**-1 strain, comprising: contacting a biological sample collected from a patient, with antibodies of claim 20, and detecting the immunological complexes formed between the **HIV**-1 antigens which may be present in the biological sample and said antibodies.

23. A method of in vitro diagnosis of a Group O **HIV**-1 strain, comprising: contacting a biological sample collected from a patient, with antibodies of claim 21, and detecting the immunological complexes formed between the **HIV**-1 antigens which may be present in the biological sample and said antibodies.

24. A diagnostic reagent for a Group O **HIV**-1, comprising at least one peptide encoded by a nucleotide selected from the group consisting of SEQ ID NO. 26, SEQ ID NO. 27, SEQ ID NO. 28, SEQ ID NO. 29, SEQ ID NO. 30, SEQ ID NO. 31, SEQ ID NO. 32, SEQ ID NO. 33, SEQ ID NO. 34, SEQ ID NO. 35, SEQ ID NO. 62, SEQ ID NO. 63, SEQ ID NO. 64, SEQ ID NO. 65, SEQ ID NO. 36, SEQ ID NO. 37, SEQ ID NO. 38, SEQ ID NO. 39, SEQ ID NO. 40, SEQ ID NO. 41, SEQ ID NO. 42, SEQ ID NO. 66, SEQ ID NO. 67, SEQ ID NO. 68, SEQ ID NO. 69, SEQ ID NO. 43, SEQ ID NO. 44, SEQ ID NO. 45, SEQ ID NO. 46, SEQ ID NO. 47, SEQ ID NO. 48, SEQ ID NO. 49, SEQ ID NO. 70, SEQ ID NO. 71, SEQ ID NO. 72, and SEQ ID NO. 73.

L11 ANSWER 20 OF 21 USPATFULL on STN
1998:157112 Methods for sensitive detection of reverse transcriptase.
Heneine, Walid, Decatur, GA, United States
Folks, Thomas M., Lithonia, GA, United States
Switzer, William Marshall, Stone Mountain, GA, United States
Yamamoto, Shinji, Decatur, GA, United States
The United States of America as represented by the Department of Health and Human Services, Washington, DC, United States (U.S. government)
US 5849494 19981215
APPLICATION: US 1996-763762 19961211 (8)

DOCUMENT TYPE: Utility; Granted.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention provides a method for detecting the presence of a retrovirus in a biological sample comprising the steps of: a) contacting the biological sample with an RNA template and a complementary DNA primer under conditions whereby the RNA template and the DNA primer will anneal and a DNA strand will be synthesized as an extension from the DNA primer if reverse transcriptase is present in the sample; b) amplifying the synthesized DNA; and c) detecting the amplification of the synthesized DNA, the amplification of the synthesized DNA indicating the presence of reverse transcriptase in the biological sample, thus indicating the presence of a retrovirus in the biological sample.
CLM What is claimed is:
1. A method for differentiating between infection by **human immunodeficiency virus**-1 Group M and Group O in a **human immunodeficiency virus**-1 infected subject comprising the steps of: a) contacting a biological sample from the subject with a ribonucleotide that is a region of the encephalomyocarditis virus genome as an RNA template, a Group M reverse transcriptase inhibiting amount of nevirapine and a oligonucleotide that is a complementary DNA primer under conditions whereby the oligonucleotide and the ribonucleotide will anneal and a DNA strand will be synthesized as an extension from the oligonucleotide if reverse transcriptase in the sample is not inhibited by the nevirapine; b) amplifying the synthesized DNA; and c) detecting the amplification of the synthesized DNA, the amplification of the synthesized DNA indicating the presence of **human immunodeficiency virus**-1 Group O in the sample.

2. A method for differentiating between infection by **human immunodeficiency virus**-1 Group M and Group O in a **human immunodeficiency virus**-1 infected subject comprising the steps of: a) contacting a biological sample from the subject with a ribonucleotide of SEQ ID NO:4, an oligonucleotide of SEQ ID NO:2 and a Group M reverse transcriptase inhibiting amount of nevirapine under conditions whereby the oligonucleotide and the ribonucleotide will anneal and a DNA strand will be synthesized as an extension from the oligonucleotide if reverse transcriptase in the sample is not inhibited by the nevirapine; b) amplifying the synthesized DNA by the polymerase chain reaction whereby the conditions of the amplification comprise about 35 cycles of heating the synthesized DNA and a primer pair consisting of the oligonucleotide of SEQ ID NO:10 and the oligonucleotide of SEQ ID NO:2 to about 95° C. for one minute, about 55° C. for one minute and about 72° C. for one minute; and detecting the amplification of the synthesized DNA, the amplification of the synthesized DNA indicating the presence of **human immunodeficiency virus**-1 Group O in the sample.

L11 ANSWER 21 OF 21 USPATFULL on STN
97:9897 Oliconucleotide primers and probes for the detection of **HIV**-1.
Respess, Richard A., Alameda, CA, United States
Hoffmann-La Roche Inc., Nutley, NJ, United States (U.S. corporation)
US 5599662 19970204
APPLICATION: US 1995-390192 19950217 (8)
DOCUMENT TYPE: Utility; Granted.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention provides improved primers for the polymerase chain reaction (PCR) amplification of a nucleic acid sequence from the pol gene of the **human immunodeficiency virus** type 1 (**HIV**-1). The invention also provides improved probes for the detection of the nucleic acid amplified using the primers of the invention. The primers and amplification methods of the invention enable the detection of **HIV**-1 from any of the known subtypes. The probes of the invention enable simple and rapid hybridization detection assays for detecting amplified **HIV**-1 nucleic acid.
CLM What is claimed is:
1. A pair of oligonucleotide primers consisting of RAR1032 (SEQ ID NO:

1) and RAR1033 (SEQ ID NO: 2).

2. A pair of oligonucleotide primers consisting of RAR1035 (SEQ ID NO: 3), and RAR1036 (SEQ ID NO: 4).

3. An oligonucleotide probe for the detection of **human immunodeficiency virus** nucleic acid, wherein said oligonucleotide probe consists of a subsequence of RAR1037 (SEQ ID NO: 6) comprising bases 7 through 35, or the complement thereof.

4. An oligonucleotide probe of claim 3 which is selected from the group consisting of RAR1037 (SEQ ID NO: 6), RAR1037T (SEQ ID NO: 8), and the complements thereof.

5. A kit for detecting **human immunodeficiency virus** type 1 (**HIV**-1) nucleic acid, wherein said kit comprises a pair of oligonucleotide primers of claim 1.

6. A kit for detecting **human immunodeficiency virus** type 1 (**HIV**-1) nucleic acid, wherein said kit comprises a pair of oligonucleotide primers of claim 2.

7. A kit of claim 5, further comprising an oligonucleotide probe consisting of a subsequence of RAR1034 (SEQ ID NO: 5) comprising bases 7 through 35, or the complement thereof.

8. A kit of claim 6, further comprising an oligonucleotide probe consisting of a subsequence of RAR1037 (SEQ ID NO: 6) comprising bases 7 through 35, or the complement thereof.

9. A method for detecting **human immunodeficiency virus** type 1 (**HIV**-1) nucleic acid, wherein said method comprises: (a) carrying out a polymerase chain reaction using a pair of oligonucleotide primers of claim 1; and (b) detecting amplified **HIV**-1 nucleic acid.

10. A method of claim 9, wherein step (b) is carried out using an oligonucleotide probe consisting of a subsequence of RAR1034 (SEQ ID NO: 5) comprising bases 7 through 35, or the complement thereof.

11. A method for detecting **human immunodeficiency virus** type 1 (**HIV**-1) nucleic acid, wherein said method comprises: (a) carrying out a polymerase chain reaction using a pair of oligonucleotide primers of claim 2; and (b) detecting amplified **HIV**-1 nucleic acid.

12. A method of claim 11, wherein step (b) is carried out using an oligonucleotide probe consisting of a subsequence of RAR1037 (SEQ ID NO: 6) comprising bases 7 through 35, or the complement thereof.

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     (FILE 'HOME' ENTERED AT 20:50:07 ON 19 FEB 2004)

     FILE 'USPATFULL' ENTERED AT 20:50:23 ON 19 FEB 2004

     FILE 'USPATFULL' ENTERED AT 20:50:50 ON 19 FEB 2004
                E BRUST STEFAN/IN
L1             13 S E3
L2              0 S 6335158/PN
L3              1 S US6335158/PN
                E KNAPP STEFAN/IN
L4             24 S E3
L5             16 S L4 NOT L1
                E GERKEN MANFRED/IN
L6             10 S E3
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L7            7 S L6 NOT (L1 OR L4)
L8        30918 S (HIV OR HUMAN IMMUNODEFICIENCY VIRUS)
L9          106 S L8 AND (MVP?)
L10          27 S L9 AND (MVP5180?)
L11          21 S L10 NOT (L1 OR L4 OR L6)

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COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                      ENTRY    SESSION
FULL ESTIMATED COST                                  149.42     150.98

FILE 'MEDLINE' ENTERED AT 21:01:46 ON 19 FEB 2004

 FILE LAST UPDATED: 19 FEB 2004 (20040219/UP).  FILE COVERS 1958 TO DATE.

 On December 14, 2003, the 2004 MeSH terms were loaded.  See HELP RLOAD
 for details.

 MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the
 MeSH 2004 vocabulary.  See http://www.nlm.nih.gov/mesh/ and
 http:\\www.nih.gov/pubs/yechbull/nd03/nd03_mesh.html for a description
 on changes.

 This file contains CAS Registry Numbers for easy and accurate
 substance identification.

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E1            1     BRUST R JR/AU
E2            5     BRUST R W JR/AU
E3            7 --> BRUST S/AU
E4            1     BRUST S E/AU
E5            1     BRUST S H/AU
E6            1     BRUST SUSAN/AU
E7            1     BRUST T A/AU
E8            1     BRUST TYSON B/AU
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              1 "BRUST S H"/AU
L12           9 ("BRUST S"/AU OR "BRUST S E"/AU OR "BRUST S H"/AU)

=> d l12,ti,1-9

L12  ANSWER 1 OF 9      MEDLINE on STN
TI   Shortening of the diagnostic window with a new combined HIV p24 antigen
     and anti-HIV-1/2/O screening test.

L12  ANSWER 2 OF 9      MEDLINE on STN
TI   Diversity of the immunodominant epitope of gp41 of HIV-1 subtype O and its
     validity for antibody detection.

L12  ANSWER 3 OF 9      MEDLINE on STN
TI   Multicentre study for diagnostic evaluation of an assay for simultaneous
     detection of antibodies to HIV-1, HIV-2 and HIV-1 subtype 0 (HIV-0).

L12  ANSWER 4 OF 9      MEDLINE on STN
TI   Reactivity of five anti-HIV-1 subtype O specimens with six different
     anti-HIV screening ELISAs and three immunoblots.

L12  ANSWER 5 OF 9      MEDLINE on STN
TI   Antigen-gelonin conjugates. Preparation and application in experimental
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myasthenia gravis.

L12 ANSWER 6 OF 9 MEDLINE on STN
TI Avian v-myc replaces chromosomal translocation in murine plasmacytomagenesis.

L12 ANSWER 7 OF 9 MEDLINE on STN
TI Rapid induction of plasmacytomas in mice by pristane and a murine recombinant retrovirus containing an avian v-myc and a defective raf oncogene.

L12 ANSWER 8 OF 9 MEDLINE on STN
TI Chromosomal radiosensitivity during G2 phase and susceptibility to plasmacytoma induction in mice.

L12 ANSWER 9 OF 9 MEDLINE on STN
TI [The work of a nurse in child and adolescent psychiatry with disturbed children].
Der Arbeitsbereich der Schwester in der Kinder- und Jugendpsychiatrie bei verhaltensgestorten Kindern.

=> d l12,cbib,ab,1-4

L12 ANSWER 1 OF 9 MEDLINE on STN
2001061332 Document Number: 20519679. PubMed ID: 11064116. Shortening of the diagnostic window with a new combined HIV p24 antigen and anti-HIV-1/2/O screening test. **Brust S**; Duttmann H; Feldner J; Gurtler L; Thorstensson R; Simon F. (Dade Behring Marburg GmbH, Marburg, Germany.) JOURNAL OF VIROLOGICAL METHODS, (2000 Nov) 90 (2) 153-65. Journal code: 8005839. ISSN: 0166-0934. Pub. country: Netherlands. Language: English.
AB Because antibodies to the human immunodeficiency virus (HIV) are absent in the very early phase of HIV infection, there remains a slight residual risk for HIV transmission by blood donations by viremic but antibody negative donations. To shorten the diagnostic window between infection and the detection of antibodies, Enzygnost HIV Integral (Dade Behring, Germany) was developed. With this new test, HIV p24 antigen and HIV antibodies can be detected simultaneously in a single test. In a multicenter study the new screening assay has been compared with various tests that detect only HIV antibodies or HIV p24 antigen and with assays which permit a simultaneous detection of HIV antigen and HIV antibodies. The new assay showed 100% sensitivity for the detection of antibodies to HIV-1, groups M (n=1102) and O (n=55), and HIV-2 (n=289). In 23 out of 52 seroconversion panels, seroconversion was detected 2-18 days earlier with the new combined antigen/antibody test compared to single antibody tests. All samples from a viral load panel (n=451), all samples containing p24 antigen (n=302), and all but one of the cell culture supernatants (n=38) infected with various HIV-1 subtypes or HIV-2 were identified reliably by the new test. The specificity of the assay for 4002 unselected blood donors was 99.78% initially and 99.80% after retesting. Potentially interfering factors had no systematic influence on specificity. By testing for p24 antigen, which is present prior to the onset of antibody production in some cases of recent HIV infection, the new assay reduces the diagnostic window as compared to third generation screening assays, thus permitting an earlier diagnosis of HIV infection.

L12 ANSWER 2 OF 9 MEDLINE on STN
97418745 Document Number: 97418745. PubMed ID: 9274821. Diversity of the immunodominant epitope of gp41 of HIV-1 subtype O and its validity for antibody detection. Eberle J; Loussert-Ajaka I; **Brust S**; Zekeng L; Hauser P H; Kaptue L; Knapp S; Damond F; Saragosti S; Simon F; Gurtler L G. (Pettenkofer Institute, University of Munchen, Germany.) JOURNAL OF VIROLOGICAL METHODS, (1997 Aug) 67 (1) 85-91. Journal code: 8005839. ISSN: 0166-0934. Pub. country: Netherlands. Language: English.
AB The immunodominant regions of the gp41 from 13 HIV-1 subtype O strains from Cameroon, 11 from France and one from Germany were sequenced. The

amino acid sequences were compared to those of the 3 published HIV-1 subtype O isolates, ANT70, MVP-5180 and VAU. All HIV-1 subtype O isolates had a very conserved amino acid sequence in this region and showed a subtype O specific structure. Within the cysteine loop there was a positive charge of two basic amino acids, arginine and lysine. Only two strains (CM.6778 and CM.8161) showed an acidic amino acid in this loop. None of the isolates showed the same amino acid sequence in this immunodominant region. A 25 residue peptide from the immunodominant domain of gp41 of the MVP-5180 strain was synthesized, cycled to form the cysteine-loop and coated to microtiter plates. Antibody binding was detected by indirect ELISA using an enzyme labeled anti-human IgG. Out of 111 anti-HIV-1 positive specimens, collected mainly from Cameroonian HIV infected patients, only 10 were not reactive in this assay. The 42 anti-HIV-1 subtype O positive specimens gave all a reaction above cut off. Despite the diversity found in the amino acid sequences within the 25 isolates a peptide-based indirect ELISA representing the immunodominant epitope of the strain MVP-5180 successfully detected all the anti-HIV-O sera so far tested, pointing to the importance of adding such a peptide for correct identification of HIV-1 subtype O infected patients, while some assays without HIV-O specific antigens partially fail to detect all anti-HIV-O specimens.

L12 ANSWER 3 OF 9 MEDLINE on STN

96128601 Document Number: 96128601. PubMed ID: 8557399. Multicentre study for diagnostic evaluation of an assay for simultaneous detection of antibodies to HIV-1, HIV-2 and HIV-1 subtype 0 (HIV-0). Bachmann P; Beyer J; **Brust S**; Engelhardt W; Gurtler L G; Habermehl K O; Karakassopoulos A; Michl U; Muhlbacher A; Stoffler-Meilicke M; +. (Swiss Red Cross, Central Laboratory, Bern, Switzerland.) INFECTION, (1995 Sep-Oct) 23 (5) 322-33. Journal code: 0365307. ISSN: 0300-8126. Pub. country: GERMANY: Germany, Federal Republic of. Language: English.

AB The aim of the study was to evaluate a new ELISA for detection of HIV-1, HIV-2 and HIV-1 subtype 0 (HIV-0) antibodies. The assay format is based on the antigen sandwich principle. To enable specific detection of HIV-0 antibodies, in addition to HIV-1 and HIV-2 antigens HIV-0 antigen is used for coating the solid phase and for the conjugate. The results show that all 12 HIV-0 samples tested were detected with a high degree of reactivity, as were all the 1,144 anti-HIV-1 and 424 anti-HIV-2 positive samples. The capacity of the test to enable early detection of seroconversions is equivalent to that of other sandwich ELISAs. The specificity of the assay was determined to be 99.89/99.94% (initial/after retest) using 58,366 samples, which is superior to the other ELISAs used for comparison. Even with difficult samples (i.e. samples of African origin, samples known to cause false-positive reactivity in different ELISAs, or samples containing potential interference factors) there were very few false-positive reactions. Therefore, the new assay is well suited for screening blood donations as well as for evaluating samples from patients of different geographic origin.

L12 ANSWER 4 OF 9 MEDLINE on STN

95256388 Document Number: 95256388. PubMed ID: 7537751. Reactivity of five anti-HIV-1 subtype O specimens with six different anti-HIV screening ELISAs and three immunoblots. Gurtler L G; Zekeng L; Simon F; Eberle J; Tsague J M; Kaptue L; **Brust S**; Knapp S. (Max von Pettenkofer Institute, University of Munich, Germany.) JOURNAL OF VIROLOGICAL METHODS, (1995 Feb) 51 (2-3) 177-83. Journal code: 8005839. ISSN: 0166-0934. Pub. country: Netherlands. Language: English.

AB Five anti-subtype O specimens were tested by anti-HIV-1/2 screening and confirmatory assays. They can be divided into three specimens, reactive with all ELISAs, independent of the nature of the antigen (recombinant proteins or peptides) and test configuration (indirect ELISA or double antigen/sandwich ELISA). One specimen was not detected by one peptide based ELISA. One specimen was only recognized by two ELISAs and should be considered as a marker sample for the weakness of currently used ELISAs with anti-subtype O. Three different immunoblot assays available commercially detected two of the specimens with a major binding of gp160

and other viral bands, especially the integrase and reverse transcriptase. Another two specimens lacked reactivity with glycoproteins almost completely, but showed some staining with the enzymes of HIV, and would most probably be interpreted as indeterminate. The fifth specimen, which was also missed by most of the ELISAs, had very faint staining of the gp160 and a very weak staining of p24, and would most probably be interpreted as negative. Adaption of currently available tests to anti-subtype O is needed for the future reliability of anti-HIV diagnostic reagents.

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     FILE 'USPATFULL' ENTERED AT 20:50:23 ON 19 FEB 2004

     FILE 'USPATFULL' ENTERED AT 20:50:50 ON 19 FEB 2004
                E BRUST STEFAN/IN
L1           13 S E3
L2            0 S 6335158/PN
L3            1 S US6335158/PN
                E KNAPP STEFAN/IN
L4           24 S E3
L5           16 S L4 NOT L1
                E GERKEN MANFRED/IN
L6           10 S E3
L7            7 S L6 NOT (L1 OR L4)
L8        30913 S (HIV OR HUMAN IMMUNODEFICIENCY VIRUS)
L9          106 S L8 AND (MVP?)
L10          27 S L9 AND (MVP5180?)
L11          21 S L10 NOT (L1 OR L4 OR L6)

     FILE 'MEDLINE' ENTERED AT 21:01:46 ON 19 FEB 2004
                E BRUST S/AU
L12           9 S E3-E5

=> e knapp s/au
E1            1      KNAPP ROY M/AU
E2            1      KNAPP RUDOLF/AU
E3          156 --> KNAPP S/AU
E4           10      KNAPP S A/AU
E5            6      KNAPP S C/AU
E6            1      KNAPP S D/AU
E7           46      KNAPP S E/AU
E8            2      KNAPP S F/AU
E9           14      KNAPP S J/AU
E10           2      KNAPP S K/AU
E11           1      KNAPP S L/AU
E12           5      KNAPP SAMUEL/AU

=> s e3
L13         156 "KNAPP S"/AU

=> s l13 and (HIV or human immunodeficiency virus)
        133820 HIV
       8386901 HUMAN
        111815 IMMUNODEFICIENCY
        363747 VIRUS
         42134 HUMAN IMMUNODEFICIENCY VIRUS
                  (HUMAN(W)IMMUNODEFICIENCY(W)VIRUS)
L14           6 L13 AND (HIV OR HUMAN IMMUNODEFICIENCY VIRUS)

=> s l14 not l12
L15           4 L14 NOT L12
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=> d l15,ti,1-4

L15  ANSWER 1 OF 4      MEDLINE on STN
TI   Highly active antiretroviral therapy responders exhibit a phenotypic
     lymphocyte pattern comparable to that of long-term nonprogressors.

L15  ANSWER 2 OF 4      MEDLINE on STN
TI   Risk management and life-threatening patient behaviors.

L15  ANSWER 3 OF 4      MEDLINE on STN
TI   A case of HIV-associated cerebral histoplasmosis successfully treated
     with fluconazole.

L15  ANSWER 4 OF 4      MEDLINE on STN
TI   A new subtype of human immunodeficiency virus type 1 (MVP-5180) from
     Cameroon.


=> d l15,cbib,ab,4

L15  ANSWER 4 OF 4      MEDLINE on STN
94149848  Document Number: 94149848.    PubMed ID: 8107219.   A new subtype of
     human immunodeficiency virus type 1 (MVP-5180) from Cameroon.
     Gurtler L G; Hauser P H; Eberle J; von Brunn A; Knapp S; Zekeng L;
     Tsague J M; Kaptue L. (Max von Pettenkofer Institute, University of
     Munich, Germany. ) JOURNAL OF VIROLOGY, (1994 Mar) 68 (3) 1581-5. Journal
     code: 0113724. ISSN: 0022-538X. Pub. country: United States. Language:
     English.
AB   A new subtype (MVP-5180) of human immunodeficiency virus type 1
     (HIV-1) was isolated from a Cameroonian AIDS patient. MVP-5180 was
     grown in several human T-cell lines and the monocytic U937 line. MVP-5180
     DNA could not be amplified by nested primer PCR with conventional env
     primers and could be only very faintly amplified with gag and pol primers.
     Most German, Ivoirian, and Malawian anti-HIV-1 sera reacted faintly or
     moderately with Env proteins in an MVP-5180 immunoblot, whereas some
     Cameroonian sera reacted strongly. Of HIV-1-infected Cameroonians, 8%
     were identified by serological methods as infected with MVP-5180; 7% were
     positive when MVP-5180-specific PCR env primers were used. DNA sequence
     analysis of MVP-5180 showed that its genetic organization was that of
     HIV-1, with 65% similarity to HIV-1 and 56% similarity to HIV-2
     consensus sequences. The env gene of MVP-5180 had similarities to HIV-1
     and HIV-2 of 53 and of 49%, respectively. V3 loop analysis identified a
     crown of Gly-Pro-Met-Arg by using cloned DNA and Gly-Pro-Leu-Arg by using
     PCR-amplified DNA, neither of which configuration has been described for
     other HIV strains. In an analysis of relationships, MVP-5180 occupied a
     position distant to all other HIV-1 strains, including the chimpanzee
     simian immunodeficiency virus type 1 SIVcpz and the Uganda virus U455, and
     closer to the HIV-1/HIV-2 divergence node. MVP-5180, together with
     another Cameroonian isolate, ANT-70, constitutes a group subtype O of the
     most divergent HIV-1 isolates yet identified. Characterization of
     MVP-5180 is important for understanding the natural history of the primate
     immunodeficiency viruses and for the development of vaccines and
     diagnostics.


=> d his

     (FILE 'HOME' ENTERED AT 20:50:07 ON 19 FEB 2004)

     FILE 'USPATFULL' ENTERED AT 20:50:23 ON 19 FEB 2004

     FILE 'USPATFULL' ENTERED AT 20:50:50 ON 19 FEB 2004
               E BRUST STEFAN/IN
L1            13 S E3
L2             0 S 6335158/PN
L3             1 S US6335158/PN
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                E KNAPP STEFAN/IN
L4            24 S E3
L5            16 S L4 NOT L1
                E GERKEN MANFRED/IN
L6            10 S E3
L7             7 S L6 NOT (L1 OR L4)
L8         30918 S (HIV OR HUMAN IMMUNODEFICIENCY VIRUS)
L9           106 S L8 AND (MVP?)
L10           27 S L9 AND (MVP5180?)
L11           21 S L10 NOT (L1 OR L4 OR L6)

     FILE 'MEDLINE' ENTERED AT 21:01:46 ON 19 FEB 2004
                E BRUST S/AU
L12            9 S E3-E5
                E KNAPP S/AU
L13          156 S E3
L14            6 S L13 AND (HIV OR HUMAN IMMUNODEFICIENCY VIRUS)
L15            4 S L14 NOT L12

=> e gerken m/au
E1             3      GERKEN LOUANN/AU
E2             2      GERKEN LUIZ MARCIO/AU
E3            27 --> GERKEN M/AU
E4             3      GERKEN M E/AU
E5             3      GERKEN M V/AU
E6             1      GERKEN MANFRED/AU
E7             1      GERKEN MARTINA/AU
E8            10      GERKEN MICHAEL/AU
E9             1      GERKEN P/AU
E10           14      GERKEN S/AU
E11           14      GERKEN S C/AU
E12           17      GERKEN S E/AU

=> s e3-e5
           27 "GERKEN M"/AU
            3 "GERKEN M E"/AU
            3 "GERKEN M V"/AU
L16        33 ("GERKEN M"/AU OR "GERKEN M E"/AU OR "GERKEN M V"/AU)

=> s l16 not (l12 or l13)
L17        33 L16 NOT (L12 OR L13)

=> s l17 and (HIV or human immunodeficiency virus)
      133820 HIV
     8386901 HUMAN
      111815 IMMUNODEFICIENCY
      363747 VIRUS
       42134 HUMAN IMMUNODEFICIENCY VIRUS
                (HUMAN(W)IMMUNODEFICIENCY(W)VIRUS)
L18         0 L17 AND (HIV OR HUMAN IMMUNODEFICIENCY VIRUS)

=> s (HIV or human immunodeficiency virus)
      133820 HIV
     8386901 HUMAN
      111815 IMMUNODEFICIENCY
      363747 VIRUS
       42134 HUMAN IMMUNODEFICIENCY VIRUS
                (HUMAN(W)IMMUNODEFICIENCY(W)VIRUS)
L19   138514 (HIV OR HUMAN IMMUNODEFICIENCY VIRUS)

=> s l19 and (MVP?)
        1094 MVP?
L20       15 L19 AND (MVP?)

=> d his
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     (FILE 'HOME' ENTERED AT 20:50:07 ON 19 FEB 2004)

     FILE 'USPATFULL' ENTERED AT 20:50:23 ON 19 FEB 2004

     FILE 'USPATFULL' ENTERED AT 20:50:50 ON 19 FEB 2004
                 E BRUST STEFAN/IN
L1             13 S E3
L2              0 S 6335158/PN
L3              1 S US6335158/PN
                E KNAPP STEFAN/IN
L4             24 S E3
L5             16 S L4 NOT L1
                E GERKEN MANFRED/IN
L6             10 S E3
L7              7 S L6 NOT (L1 OR L4)
L8          30918 S (HIV OR HUMAN IMMUNODEFICIENCY VIRUS)
L9            106 S L8 AND (MVP?)
L10            27 S L9 AND (MVP5180?)
L11            21 S L10 NOT (L1 OR L4 OR L6)

     FILE 'MEDLINE' ENTERED AT 21:01:46 ON 19 FEB 2004
                 E BRUST S/AU
L12             9 S E3-E5
                E KNAPP S/AU
L13           156 S E3
L14             6 S L13 AND (HIV OR HUMAN IMMUNODEFICIENCY VIRUS)
L15             4 S L14 NOT L12
                E GERKEN M/AU
L16            33 S E3-E5
L17            33 S L16 NOT (L12 OR L13)
L18             0 S L17 AND (HIV OR HUMAN IMMUNODEFICIENCY VIRUS)
L19        138514 S (HIV OR HUMAN IMMUNODEFICIENCY VIRUS)
L20            15 S L19 AND (MVP?)

=> s l20 not (l12 or l13)
L21            13 L20 NOT (L12 OR L13)

=> d l21,ti,1-13

L21  ANSWER 1 OF 13      MEDLINE on STN
TI   Differential dependence of the infectivity of HIV-1 group O isolates on
     the cellular protein cyclophilin A.

L21  ANSWER 2 OF 13      MEDLINE on STN
TI   Phylogenetic analysis of protease and transmembrane region of HIV type 1
     group O.

L21  ANSWER 3 OF 13      MEDLINE on STN
TI   Interpatient genetic variability of HIV-1 group O.

L21  ANSWER 4 OF 13      MEDLINE on STN
TI   Tropism, coreceptor use, and phylogenetic analysis of both the V3 loop and
     the protease gene of three novel HIV-1 group O isolates.

L21  ANSWER 5 OF 13      MEDLINE on STN
TI   Evaluation of different V3 peptides in an enzyme immunoassay for specific
     HIV type 1 group O antibody detection.

L21  ANSWER 6 OF 13      MEDLINE on STN
TI   Envelope sequence variability and serologic characterization of HIV type
     1 group O isolates from equatorial guinea.

L21  ANSWER 7 OF 13      MEDLINE on STN
TI   Geographical distribution of HIV-1 group O viruses in Africa.

L21  ANSWER 8 OF 13      MEDLINE on STN
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TI Complement activation by **HIV**-1-infected cells: the role of transmembrane glycoprotein gp41.

L21 ANSWER 9 OF 13 MEDLINE on STN
TI Epidemiological and molecular characteristics of **HIV** infection in Gabon, 1986-1994.

L21 ANSWER 10 OF 13 MEDLINE on STN
TI Fast analysis of genomic homologies: primate immunodeficiency virus.

L21 ANSWER 11 OF 13 MEDLINE on STN
TI Surveillance for **human immunodeficiency virus** type 1 group O infections in the United States.

L21 ANSWER 12 OF 13 MEDLINE on STN
TI New crown motif of an **HIV**-1 V3 loop sequence from a Ugandan AIDS patient.

L21 ANSWER 13 OF 13 MEDLINE on STN
TI Genotypic subtypes of **HIV**-1 in Cameroon.

=> d l21,cbib,ab,1-13

L21 ANSWER 1 OF 13 MEDLINE on STN
2002269476 Document Number: 22008475. PubMed ID: 12009870. Differential dependence of the infectivity of **HIV**-1 group O isolates on the cellular protein cyclophilin A. Wiegers Klaus; Krausslich Hans-Georg. (Heinrich-Pette-Institut fur Experimentelle Virologie und Immunologie an der Universitat Hamburg, Hamburg, D-20251, Germany.. wiegers@hpi.uni-hamburg.de) . VIROLOGY, (2002 Mar 15) 294 (2) 289-95. Journal code: 0110674. ISSN: 0042-6822. Pub. country: United States. Language: English.
AB The cellular protein Cyclophilin A (Cyp A) is packaged into **human immunodeficiency virus** type 1 (**HIV**-1) particles through a specific interaction with the capsid domain of the Gag polyprotein. Inhibition of Cyp A incorporation by mutagenesis or cyclosporin treatment severely affects infectivity of all **HIV**-1 M subtypes tested. In contrast, the closely related lentiviruses **HIV**-2 and simian immunodeficiency virus (SIV) do not package Cyp A and are not inhibited by cyclosporin. For the **HIV**-1 group O isolate **MVP5180**, it was found that Cyp A incorporation and Cyp A dependence of infectivity did not correlate. This virus incorporates Cyp A but is not sensitive to treatment with cyclosporin A. For a more detailed study concerning the relationship between Cyp A incorporation and Cyp A dependence, we have analyzed five group O isolates for their ability to incorporate Cyp A and their sensitivity to cyclosporin treatment. All group O viruses incorporated Cyp A in comparable amounts as the M-group **HIV**-1 strain NL4-3. Furthermore, Cyp A incorporation was inhibited by cyclosporin in all cases. However, while isolate **MVP** 5180 was confirmed to replicate independent of Cyp A, three of the other four isolates were sensitive to cyclosporin treatment. Sequence analysis of the Cyp A binding regions revealed that the proline-rich motif, which is responsible for Cyp A incorporation, was conserved in all four isolates, while some sequence variations were detected in other positions close to this region. These results suggest that Cyp A dependence of replication is influenced by regions outside the Cyp-binding loop and may aid in determination of Cyp A function in **HIV**-1 replication.

L21 ANSWER 2 OF 13 MEDLINE on STN
2001032154 Document Number: 20386754. PubMed ID: 10933623. Phylogenetic analysis of protease and transmembrane region of **HIV** type 1 group O. Yang C; Gao F; Funjungo P N; Zekeng L; van der Groen G; Pieniazek D; Schable C; Lal R B. (HIV Immunology and Diagnostics Branch, Division of AIDS, STD, and TB Laboratory Research, NCID, Atlanta, Georgia 30333, USA.) AIDS RESEARCH AND HUMAN RETROVIRUSES, (2000 Jul 20) 16 (11) 1075-81. Journal code: 8709376. ISSN: 0889-2229. Pub. country: United States. Language: English.

AB The molecular diversity and phylogenetic relationship of 22 **HIV**-1 group O strains were examined on the basis of the protease gene and the N-terminal region of gp41env. Analysis of the newly characterized protease sequences with 12 reference sequences revealed no specific clustering patterns, despite the distinct geographic locations of the specimens. In contrast, analysis of the newly sequenced gp41 sequences with 34 published sequences revealed two distinct clusters, each represented by one full-length sequence (**MVP5180** and ANT-70). Further, four of the specimens classified as group O in the protease region clustered with group M in the gp41 region (three subtype A and one subtype G, respectively), suggesting dual and/or recombinant infections with **HIV**-1 groups M and O. The presence of two distinct clusters in the gp41 region indicates at least two possible subtypes within group O viruses, and this may provide useful information regarding molecular epidemiological studies of group O infections.

L21 ANSWER 3 OF 13 MEDLINE on STN
1999223950 Document Number: 99223950. PubMed ID: 10207543. Interpatient genetic variability of **HIV**-1 group O. Janssens W; Heyndrickx L; Van der Auwera G; Nkengasong J; Beirnaert E; Vereecken K; Coppens S; Willems B; Fransen K; Peeters M; Ndumbe P; Delaporte E; van der Groen G. (Department of Microbiology, Institute of Tropical Medicine, Antwerp, Belgium.) AIDS, (1999 Jan 14) 13 (1) 41-8. Journal code: 8710219. ISSN: 0269-9370. Pub. country: ENGLAND: United Kingdom. Language: English.
AB OBJECTIVE: To analyse the genetic and phylogenetic characteristics of **HIV**-1 group O viruses. MATERIALS AND METHODS: The env gene, encoding the gp160 glycoprotein, and a partial p24-encoding gag gene fragment of a Cameroonian (CA9) and a Gabonese (VI686) **HIV**-1 group O virus, isolated from cultured peripheral blood mononuclear cells of symptomatic patients, were sequenced, aligned with other representatives of group O for which the same region has been documented, and genetically and phylogenetically analysed. RESULTS: Phylogenetic analysis of the env gene (gp160) revealed that CA9, VI686, ANT70, and four Ha strains formed a separate cluster, which was supported by 100% of all bootstrap trees. In addition, these seven isolates were part of the same clade in the p24 phylogeny. VAU and **MVP5180** may represent two other subtypes. CONCLUSION: We have characterized two group O viruses, originating from Cameroon and Gabon, which show a close evolutionary relationship to ANT70 and four Ha strains based on the entire env gene, suggestive of a first group O subgroup, tentatively named the **HIV**-1 group O env ANT70 clade or subtype.

L21 ANSWER 4 OF 13 MEDLINE on STN
1998379694 Document Number: 98379694. PubMed ID: 9715837. Tropism, coreceptor use, and phylogenetic analysis of both the V3 loop and the protease gene of three novel **HIV**-1 group O isolates. Vallejo A; Heredia A; Mas A; Lee S F; Epstein J S; Soriano V; Hewlett I K. (Laboratory of Molecular Virology, Center for Biologics Evaluation and Research, U.S. Food and Drug Administration, Bethesda, Maryland, USA.) JOURNAL OF ACQUIRED IMMUNE DEFICIENCY SYNDROMES AND HUMAN RETROVIROLOGY, (1998 Aug 15) 18 (5) 417-25. Journal code: 9501482. ISSN: 1077-9450. Pub. country: United States. Language: English.
AB **HIV**-1 has been subdivided into two groups, M and O, based on phylogenetic analysis. To better understand the pathogenesis of group O viruses, we studied biologic and genetic characteristics of two primary isolates from Spain, ES1158.1 and ES1159.1, and one from the United States, MD.1. After viral isolation, we studied the replication kinetics in peripheral blood mononuclear cells (PBMCs) and macrophages, as well as in different cell lines. All three isolates could replicate in both PBMCs and macrophages. Because no syncytium formation was detected in the MT-2 cell line, viruses were classified as non-syncytium inducing (NSI). All three isolates used the CCR5 coreceptor for entry into the human osteosarcoma (HOS) CD4 cells. Phylogenetic analysis of V3 loop sequences showed that ES1158.1 and ES1159.1 isolates were closely related to the ANT70 strain, whereas MD.1 isolate clustered with the **MVP**-5180 strain in the same branch. Interestingly, all viruses appeared to be more closely related to the **MVP**-5180 strain when the protease gene was analyzed,

although accessible sequences of this region are very limited.

L21 ANSWER 5 OF 13 MEDLINE on STN

1998349431 Document Number: 98349431. PubMed ID: 9686642. Evaluation of different V3 peptides in an enzyme immunoassay for specific **HIV** type 1 group O antibody detection. Ondoa P; Willems B; Fransen K; Nkengasong J; Janssens W; Heyndrickx L; Zekeng L; Ndumbe P; Simon F; Saragosti S; Gurtler L; Peeters M; Korber B; Goudsmit J; van der Groen G. (Institute of Tropical Medicine, Antwerp, Belgium.) AIDS RESEARCH AND HUMAN RETROVIRUSES, (1998 Jul 20) 14 (11) 963-72. Journal code: 8709376. ISSN: 0889-2229. Pub. country: United States. Language: English.

AB Strategies to discriminate group O from group M infections need to be improved. We have developed and evaluated an **HIV**-1 group O V3 peptide-based enzyme immunoassay (PEIA) for specific **HIV**-1 group O antibody detection among **HIV**-1-infected patients. Synthetic peptides, derived from the amino acid sequences of the V3 loop of 15 different group O strains and 7 group O consensus sequences, were evaluated in a PEIA against a panel of genetically confirmed group O (n = 33), group M (n = 90), and **HIV**-1 antibody-negative sera (n = 17). The best-performing PEIA(s) were then used to screen 134 sera of European and 336 sera of Cameroonian origin for the presence of anti-**HIV**-1 group O antibodies. The reactivity of reference ("gold standard") sera to individual peptides in the PEIA resulted in the selection of five different peptides with sensitivities (sens), specificities (spec), and test efficiencies (TEs) in the range of 90 to 100%. Improvement of the PEIA was obtained with simultaneous reactivity of at least two different peptides in separate wells of an ELISA plate, together with stringent criteria for positivity. We were able to select seven peptide combinations each with a sens, spec, and TE of 96.9, 100, and 99.2%, respectively. None of the 134 European and 4 (1.2%) of the 336 Cameroonian samples sera were group O positive in the optimized **HIV**-1 group O PEIA; this was confirmed by the repeated presence of reactives, in agreement with the present knowledge of group O infection distribution. Finally, we were able to develop a strategy with a higher TE (99.2%) than the previously used ANT-70 (98.5%) and ANT-70/**MVP5180** (95.7%). Our results show that optimal specificity rather than optimal sensitivity makes the V3 PEIA a sufficiently accurate epidemiological tool to be useful in estimating specifically group O infection among **HIV**-1-infected patients.

L21 ANSWER 6 OF 13 MEDLINE on STN

97407537 Document Number: 97407537. PubMed ID: 9264286. Envelope sequence variability and serologic characterization of **HIV** type 1 group O isolates from equatorial guinea. Hunt J C; Golden A M; Lund J K; Gurtler L G; Zekeng L; Obiang J; Kaptue L; Hampl H; Vallari A; Devare S G. (AIDS Research and Retrovirus Discovery, Abbott Laboratories, North Chicago, Illinois 60064, USA.) AIDS RESEARCH AND HUMAN RETROVIRUSES, (1997 Aug 10) 13 (12) 995-1005. Journal code: 8709376. ISSN: 0889-2229. Report No.: PIP-129455; POP-00272760. Pub. country: United States. Language: English.

AB Four sera from Equatorial Guinea (EG) suspected to contain antibody against **HIV**-1 group O-related viruses were identified on the basis of unusual and differential serologic reactivity in selected commercial assays and Western blot. Degenerate primers, designed from **HIV**-1 group O published sequences, were used to PCR amplify envelope (env) gene sequences from the suspect EG sera. A complete envelope gene sequence from each serum was determined from the overlapping env gene fragments. Analysis (PHYLIP package of programs) of Env amino acid sequences (translated from nucleotide sequences) indicated that the amino acid sequences obtained from EG sera clustered more closely with **HIV** Env sequences of group O compared to group M. The amino acid sequences at the octameric tip of the V3 loop were either RIGPLAWY (one isolate), RIGPMAWY (two isolates), or GLGPLAVY (one isolate). The V3 tip tetrameric sequence GPLA is represented only once in the 1995 **HIV** (Los Alamos) database, but was present in two of our group O-related EG samples. The gp41 immunodominant regions (IDR) protein sequences were identical for sequences from three of the sera, RLLALETLIQNQQLLNLWGCKGR(K)L(I)VCYTSVK(T)

W, whereas sequence from the fourth serum contained three changes as noted in parentheses. IDR sequences derived from EG sera were unique compared to those reported for other **HIV**-1 group O isolate ANT70, VAU, or **MVP5180**. Antibody in each EG serum directed against the IDR could be detected using synthetic peptides comprising sequences from the ANT70 or **MVP5180** IDRs, but were most reactive against the sequences derived from the samples themselves. Little or no serologic reactivity was detected when EG sera were reacted against peptides comprising the IDR of **HIV**-1 group M (subtype B consensus) or **HIV**-2 (consensus). The genetic variation and epidemiology of **HIV**-1 group O isolates are of considerable importance to the design of **HIV**-1 diagnostic and screening assays, especially since current serologic and genetic methods to detect **HIV**-1 have been developed mainly on the basis of sequences from isolates belonging to **HIV**-1 group M. The **HIV** envelope protein, especially the gp41 immunodominant region, plays a major antigenic role in the detection of **HIV** infection and for discriminating **HIV**-1 from **HIV**-2 antibody. This paper reports upon genetic variation and the serologic characterization of env sequences from 4 people living in Equatorial Guinea (EG) who were infected with **HIV**-1 group O. Selected commercial assays and Western blot were first used to identify the sera, then degenerate primers, designed from **HIV**-1 group O published sequences, were used to PCR amplify envelope (env) gene sequences. A complete envelope gene sequence from each serum was determined from the overlapping env gene fragments. The env amino acid sequence analysis found the EG sera sequences to be clustered more closely with the **HIV** env sequences of group O rather than to group M. The amino acid sequences at the octameric tip of the V3 loop were either RIGPLAWY, RIGPMAWY, or GLGPLAVY. Although the V3 tip tetrameric sequence GPLA is represented only once in the 1995 **HIV** database, it was present in 2 of the group O-related EG samples. The gp41 immunodominant regions (IDR) protein sequences were identical for sequences from 3 of the sera. IDR sequences derived from the EG sera were unique compared to those reported for other **HIV**-1 group O isolates ANT70, VAU, or **MVP5180**. Other findings are discussed in detail.

L21 ANSWER 7 OF 13 MEDLINE on STN

97239106 Document Number: 97239106. PubMed ID: 9084797. Geographical distribution of **HIV**-1 group O viruses in Africa. Peeters M; Gueye A; Mboup S; Bibollet-Ruche F; Ekaza E; Mulanga C; Ouedrago R; Gandji R; Mpele P; Dibanga G; Koumare B; Saidou M; Esu-Williams E; Lombart J P; Badombena W; Luo N; Vanden Haesevelde M; Delaporte E. (Laboratoire Retrovirus, ORSTOM, Montpellier, France.) AIDS, (1997 Mar 15) 11 (4) 493-8. Journal code: 8710219. ISSN: 0269-9370.

Report No.: PIP-121742; POP-00264982. Pub. country: United States.

Language: English.

AB OBJECTIVE: To determine to what extent **HIV**-1 group O strains are present in different African countries. MATERIALS AND METHODS: A total of 14,682 samples of sera from a range of patients from 12 different African countries were tested. All the sera were tested with an enzyme-linked immunosorbent assay (ELISA) using a combination of V3 peptides from ANT-70 and **MVP**-5180. Samples reactive in ELISA were retested in a line immunoassay (LIA-O). Samples reactive in ELISA were also retested with an in-house Western blot to determine the presence of antibodies to gp120 of **HIV**-1 ANT-70. Polymerase chain reaction was performed on **HIV**-1 group O and group O indeterminate sera. RESULTS: Of all the sera samples tested, only 19 sera had antibodies to group O V3 peptides exclusively and 46 were indeterminate for group O infection in LIA-O. The highest prevalence of **HIV**-1 group O infection among **HIV**-positive sera was observed in Cameroon (2.1%) and neighbouring countries, 1.1% in Nigeria and 0.9% in Gabon. The lowest rates were seen in west Africa: 0.07% in Senegal, 0.14% in Togo, 0.16% in Chad and 0.3% in Niger. Group O sera were observed in almost all the population categories tested. The ANT-70 V3 peptide in LIA-O was reactive with all of the sera considered to be **HIV**-1 group O antibody positive by LIA, versus 78.9% for the **MVP**-5180 peptide. Thirteen out of 19 group O samples of sera were tested in PCR. Eight samples were identified as group O by specific group O pol and/or V3

primers; in the remaining five samples no **HIV** RNA could be detected. Of the indeterminate sera samples, two were identified as group O. CONCLUSION: In eight of the 12 countries tested, antibodies to group O viruses were identified. Numbers of **HIV**-1 group O viruses are low. Their presence is not restricted to Cameroon and neighbouring countries but can also be found in west and south-east Africa. An enzyme-linked immunosorbent assay (ELISA), using a combination of V3 peptides and ANT-70 and **MVP**-5180, was used to test 14,682 sera samples from people living in Burkina Faso, Burundi, Cameroon, Chad, Congo, Gabon, Mali, Niger, Nigeria, Senegal, Togo, and Zambia to examine the geographic spread of **HIV**-1 group O viruses in Africa. An in-house Western blot and a line immunoassay (LIA-O) were used to detect the presence of antibodies to gp120 of **HIV**-1 ANT-70 of samples reactive in ELISA and then a polymerase chain reaction (PCR) on **HIV**-1 group O and group O indeterminant sera. **HIV**-1 group O antibodies were present in 8 countries (Cameroon, Chad, Gabon, Niger, Nigeria, Senegal, Togo, and Zambia). Among these 8 countries, the prevalence of **HIV**-1 group O sera ranged from 2.1% in Cameroon to 0.07% in Senegal. Cameroon and its neighboring countries had a higher prevalence than the West African countries (0.9-2.1% vs. 0.07-0.3%) and Zambia. **HIV**-1 group O virus was more or less evenly distributed among the population groups tested. The ANT-70 V3 peptide in LIA-O had a higher reactivity rate with **HIV**-1 group O sera than **MVP**-5180 V3 peptide in LIA-O (100% vs. 78.9%). 8 of the 13 samples tested in PCR were identified as group O by specific group O pol and/or V3 primers. Among the remaining 5 indeterminant sera samples, 2 were identified as group O. Prospective studies are needed to monitor the true prevalence of **HIV**-1 group O viruses in Cameroon, its neighboring countries, and West Africa. They are also needed to determine the risk factors associated with group O infection. Monitoring these viruses will allow adaptation of **HIV** testing strategies for blood screening and serodiagnosis if required.

L21 ANSWER 8 OF 13 MEDLINE on STN

97205214 Document Number: 97205214. PubMed ID: 9052718. Complement activation by **HIV**-1-infected cells: the role of transmembrane glycoprotein gp41. Marschang P; Kruger U; Ochsenbauer C; Gurtler L; Hittmair A; Bosch V; Patsch J R; Dierich M P. (Institut fur Hygiene, Universitat Innsbruck, Austria.) JOURNAL OF ACQUIRED IMMUNE DEFICIENCY SYNDROMES AND HUMAN RETROVIROLOGY, (1997 Feb 1) 14 (2) 102-9. Journal code: 9501482. ISSN: 1077-9450. Pub. country: United States. Language: English.

AB To characterize the mechanisms of complement activation by **human immunodeficiency virus** type 1 (**HIV**-1)-infected cells, Cl-4 cells stably expressing the envelope glycoproteins of **HIV**-1 and the parent African green monkey cell line CV-1 were tested for C1q binding and complement activation. While the parent cell line CV-1 only showed a weak spontaneous activation of the alternative pathway, Cl-4 cells additionally triggered the classical pathway of complement activation independent of anti-**HIV** antibodies by direct C1q binding. Earlier studies had shown different complement activating potential of cells infected with various **HIV** isolates. Recombinant soluble CD4-induced shedding of gp120 from the surface of **HIV**-1-infected cells converted a weak activator isolate (**MVP**-899) into a strong complement activator. The increase in complement activation was paralleled by the concomitant unmasking of a previously hidden gp41 epitope comprising the major complement-activating domain of gp41 (aa. 601-613). Our results strongly suggest that the transmembrane protein gp41 induces the activation of complement on the surface of infected cells as has been described previously for purified **HIV**-1 virions. Furthermore, we present evidence that the different potential of **HIV** isolates to activate the complement system on the cell surface is caused by different degrees of spontaneous gp120 shedding by various **HIV** isolates.

L21 ANSWER 9 OF 13 MEDLINE on STN

96426454 Document Number: 96426454. PubMed ID: 8828748. Epidemiological and molecular characteristics of **HIV** infection in Gabon, 1986-1994.

Delaporte E; Janssens W; Peeters M; Buve A; Dibanga G; Perret J L; Ditsambou V; Mba J R; Courbot M C; Georges A; Bourgeois A; Samb B; Henzel D; Heyndrickx L; Fransen K; van der Groen G; Larouze B. (AIDS Programme, Institut Francais de Recherche Scientifique pour le Developpement (ORSTOM), Montpellier, France.) AIDS, (1996 Jul) 10 (8) 903-10. Journal code: 8710219. ISSN: 0269-9370. Pub. country: United States. Language: English.

AB OBJECTIVE: To describe trends in the prevalence of **HIV**-1 infection in different populations in Gabon, and the molecular characteristics of circulating **HIV** strains. METHODS: Data were collected on **HIV** prevalence through sentinel surveillance surveys in different populations in Libreville (the capital) and in Franceville. In Libreville, a total of 7082 individuals (hospitalized patients, tuberculosis patients, pregnant women, asymptomatic adults, prisoners) were recruited between 1986 and 1994. In Franceville, we tested 771 pregnant women and 886 healthy asymptomatic adults (1986-1988). Sera were screened for **HIV** antibodies by enzyme-linked immunosorbent assay (ELISA) and confirmed by Western blot or line immunoassay (LIA). Reactive samples in ELISA were tested for the presence of antibodies to **HIV**-1 group O viruses by ELISA using V3 peptides from **HIV**-1 ANT-70 and **HIV**-1 **MVP**-5180 followed by confirmation by LIA and a specific Western blot. Seventeen **HIV**-1 strains were isolated (1988-1993) and a 900 base-pair fragment encoding the env region containing V3, V4, V5 and beginning of gp41 was sequenced and a phylogenetic tree was constructed. RESULTS: **HIV** prevalence was relatively low and remained stable (0.7-1.6% in pregnant women, 2.1-2.2% in the general population). The prevalence was also stable among prisoners (2.1-2.6%). Among hospitalized and tuberculosis patients prevalence was higher and increased (1.8-12.7% and 1.5-16.2%, respectively). Only three sera had antibodies to **HIV**-1 group O. The 17 **HIV**-1 strains represent six different genetic subtypes including type O. CONCLUSION: Our data from 1986 to 1994 show a stable and low **HIV** prevalence in Gabon, and a high genetic diversity of **HIV**-1 strains. This, also observed in Cameroon, is in contrast to that found elsewhere in Africa. Differences in rate of spread of **HIV** infection are probably explained by interplay between numerous factors. The role of different **HIV** subtypes in the dynamics of the **HIV** epidemic should be examined further.

L21 ANSWER 10 OF 13 MEDLINE on STN

96304333 Document Number: 96304333. PubMed ID: 8660432. Fast analysis of genomic homologies: primate immunodeficiency virus. Moncany M L; Courtois P R. (Laboratory of Cellular and Molecular Biology, University of La Rochelle, France.) JOURNAL OF MOLECULAR EVOLUTION, (1996 Aug) 43 (2) 152-60. Journal code: 0360051. ISSN: 0022-2844. Pub. country: United States. Language: English.

AB We have recently published a new probabilistic algorithm which performs genomic comparisons on a huge scale. In the present paper it was applied to immunodeficiency viral sequences extracted from international gene databanks. During global sequence analysis of human (HIV1 and HIV2) and simian viruses by means of dot-matrix representation, series of homology were obtained which permitted the definition of families of viruses, overlapping the species divisions. Sequences of interest were characterized to the lexical base sentence through successive zoomings. Strain-to-strain comparison confirmed subfamily classifications and led, for example, to the identification of divergent LTR sequences. By way of example, we described the application of the algorithm to the ANT70C and **MVP5180** HIV1-O viruses, for which the observed differences were shown to correspond to a deletion in the U3 region, situated between the LEF and NF-kappaB sites. It was of interest to consider these data in a tentative phylogenetic interpretation.

L21 ANSWER 11 OF 13 MEDLINE on STN

96282582 Document Number: 96282582. PubMed ID: 8693502. Surveillance for **human immunodeficiency virus** type 1 group O infections in the United States. Pau C P; Hu D J; Spruill C; Schable C; Lackritz E; Kai M; George J R; Rayfield M A; Dondero T J; Williams A E; Busch M P; Brown A E;

McCutchan F E; Schochetman G. (Division of HIV/AIDS, Centers for Disease Control and Prevention, Atlanta, Georgia, USA.) TRANSFUSION, (1996 May) 36 (5) 398-400. Journal code: 0417360. ISSN: 0041-1132. Pub. country: United States. Language: English.

AB BACKGROUND: Reports that the **human immunodeficiency virus** type 1 (**HIV**-1) group O variants are not reliably detected by some commercial diagnostic tests have raised concerns about the sensitivity of existing screening tests, especially with regard to blood safety. Although it is unlikely that these divergent strains are prevalent in North America, systematic, continuous surveillance is needed to monitor the potential spread of **HIV** variants into that region. STUDY DESIGN AND METHODS: Stored serum samples (n = 1072) from both high- and low-risk population groups at several sites in the United States and Puerto Rico were tested by peptide enzyme immunoassays specific for the prototypic **HIV**-1 group O strains, **MVP5180** and ANT70. RESULTS: None of the 1072 samples examined had peptide reactivity that was consistent with **HIV**-1 group O infection. CONCLUSION: While no evidence of specific **HIV**-1 group O (**MVP5180** or ANT70) infection was found in this study, the sensitivity of current tests has not been fully evaluated against the wide range of genetic variation of **HIV**. Therefore, it is important to continue active surveillance for **HIV**-1 and **HIV** type 2 strains, to characterize any divergent strains, and to judiciously modify tests to correct for any deficiencies in sensitivity.

L21 ANSWER 12 OF 13 MEDLINE on STN

95251931 Document Number: 95251931. PubMed ID: 7734191. New crown motif of an **HIV**-1 V3 loop sequence from a Ugandan AIDS patient. von Brunn A; von Brunn B; Eberle J; Biryahwaho B; Downing R G; Gurtler L. (Max-von-Pettenkofer-Institut, Munchen, Germany.) AIDS RESEARCH AND HUMAN RETROVIRUSES, (1995 Jan) 11 (1) 183-4. Journal code: 8709376. ISSN: 0889-2229.
Report No.: PIP-106486; POP-00246828. Pub. country: United States. Language: English.

AB **HIV**-1 V3 loop sequences from Ugandan patients include motifs from subtypes A, B, and D. To characterize further **HIV** isolates, V3 loop sequences were amplified from **HIV**-1 isolated in 1987 from peripheral blood mononuclear cells (PBL) of three patients with full-blown AIDS from Kampala, Uganda. The PBL were separated by Ficoll Paque gradients and cocultivated with noninfected donor lymphocytes for two weeks. The **HIV** was then transferred to HUT-78 cells. From extracted DNA of the permanently-infected HUT-78 cells, nested polymerase chain reaction (PCR) was conducted, with V3 loop sequencing performed directly upon PCR fragments derived from two independent DNA preparations and on cloned fragments. Isolates **MVP**-9801, -9802, and -9803 show 35.6%, 32.4%, and 29.7% nucleotide sequence divergence from the ELI subtype D sequence; 31.5%, 25.7%, and 18.9% divergence from the Z2Z6 subtype D sequence; and 21.9%, 12.2%, and 12.2% divergence from the subtype D consensus sequence. All three deduced amino acid sequences fit into the subtype D consensus sequence rather than into other V3 loop sequences described for Ugandan subtype A isolates. **MVP**-9802 and **MVP**-9803 contain the GSGQA pentapeptide motif at the tip of the V3 loop, while **MVP**-9801 contains GGRA. This may be explained by a deletion of proline codon between the codons for the two glycine residues. The authors believe that this deletion has not been previously reported. They also note that the deletion does not appear to be associated with a growth difference in vitro or with a difference in pathogenicity in vivo. The immunogenic implications of this altered V3 loop crest remain unclear. The Western blot profiles for the gp160, gp120, and gp41 proteins of the three Ugandan isolates manifest normal molecular weights.

L21 ANSWER 13 OF 13 MEDLINE on STN

95118531 Document Number: 95118531. PubMed ID: 7818811. Genotypic subtypes of **HIV**-1 in Cameroon. Nkengasong J N; Janssens W; Heyndrickx L; Fransen K; Ndumbe P M; Motte J; Leonaers A; Ngolle M; Ayuk J; Piot P; +. (Department of Infection and Immunity, Institute of Tropical Medicine, Antwerp, Belgium.) AIDS, (1994 Oct) 8 (10) 1405-12. Journal code:

8710219. ISSN: 0269-9370.
Report No.: PIP-099280; POP-00233687. Pub. country: United States.
Language: English.

AB OBJECTIVE: The only two **HIV**-1 strains (ANT70 and **MVP5180**) reported to date from Cameroon are members of the outlier clade (group O). In this study, we assessed the prevalence of group O viruses and other **HIV**-1 subtypes in Cameroon. DESIGN: A phylogenetic analysis of 18 **HIV**-1 strains isolated from seropositive individuals from Yaounde and Douala, Cameroon. METHODS: A 900 base-pair fragment of the env gene coding for V3, V4, V5, and the beginning of gp41 of 17 out of 18 **HIV**-1 isolates from Cameroon was amplified, cloned and sequenced using polymerase chain reaction. A phylogenetic tree was constructed. RESULTS: The overall env nucleotide sequence divergence among the Cameroon isolates ranged from 6.1 to 27.5%. In a phylogenetic tree, six subtypes were identified when compared with 23 reference strains of different geographic origin. Of these 17 Cameroonian strains, 11 (61%) were of subtype A of which the interpatient distances at the sequence level varied from 6.1% to 18.3% (average, 11.9%). Three (17%) strains were of subtype F, and the other three strains (6% each) belonged to subtypes B, E and H, respectively. The remaining isolate was classified as belonging to group O, on the basis of the sequence of part of the pol gene. A very broad spectrum of different tetrameric amino-acid sequences was observed at the apex of the V3 loop. Eleven strains contained the tetrameric globally predominant GPGQ sequence at the tip of the V3 motif. Two strains had the GPGR sequence typical of the American and European **HIV**-1 strains. The remaining tetrameric sequences included GPGS, GSGQ, GRGQ, and GLGR. CONCLUSION: These findings on a limited number of viruses suggest extensive env gene diversity of **HIV**-1 strains from Cameroon, and could have implications for vaccine development in Africa.

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(FILE 'HOME' ENTERED AT 20:50:07 ON 19 FEB 2004)

FILE 'USPATFULL' ENTERED AT 20:50:23 ON 19 FEB 2004

FILE 'USPATFULL' ENTERED AT 20:50:50 ON 19 FEB 2004

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                E BRUST STEFAN/IN
L1           13 S E3
L2            0 S 6335158/PN
L3            1 S US6335158/PN
                E KNAPP STEFAN/IN
L4           24 S E3
L5           16 S L4 NOT L1
                E GERKEN MANFRED/IN
L6           10 S E3
L7            7 S L6 NOT (L1 OR L4)
L8        30918 S (HIV OR HUMAN IMMUNODEFICIENCY VIRUS)
L9          106 S L8 AND (MVP?)
L10          27 S L9 AND (MVP5180?)
L11          21 S L10 NOT (L1 OR L4 OR L6)
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FILE 'MEDLINE' ENTERED AT 21:01:46 ON 19 FEB 2004

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                E BRUST S/AU
L12           9 S E3-E5
                E KNAPP S/AU
L13         156 S E3
L14           6 S L13 AND (HIV OR HUMAN IMMUNODEFICIENCY VIRUS)
L15           4 S L14 NOT L12
                E GERKEN M/AU
L16          33 S E3-E5
L17          33 S L16 NOT (L12 OR L13)
L18           0 S L17 AND (HIV OR HUMAN IMMUNODEFICIENCY VIRUS)
L19      138514 S (HIV OR HUMAN IMMUNODEFICIENCY VIRUS)
L20          15 S L19 AND (MVP?)
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L21 13 S L20 NOT (L12 OR L13)

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ALL L# QUERIES AND ANSWER SETS ARE DELETED AT LOGOFF
LOGOFF? (Y)/N/HOLD:y
STN INTERNATIONAL LOGOFF AT 21:14:50 ON 19 FEB 2004